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1 (bases 1 to 2170)
Lee,J.K., Bhakta,S., Rosen,S.D. and Characterization of a N-acetylglucosamine-6-sulfotransfintestinal tissue
Biochem. Biophys. Res. Commun. 26 99423499
2 (bases 1 to 2170)
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/ note="possibly involved in biosynthesis of mucosal
| ligands for L-selectin"
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/ protein_id="AaaD56000.1"
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RS Akama,T.O., Nishida,K., Nakayama,J., Watanabe,H., Ozaki,K., Nakamura,T., Tota, T., Shimomura,Y., Maeda,N., Yamamoto,S., Fujiwara,T., Thonar,E.J., Shimomura,Y., Kinoshita,S., Tanigami,A. macular corneal dystrophy type I and type II are caused by distinct mutations in a new sulphotransferase gene

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Direct Submission

Submitted (17-MAR-2000) Glycobiology Program, The Burnham Submitted (17-MAR-2000) flycobiology Program, The Burnham Institute, 10901 North Torrey Pines Road, La Jolla, CA 92037, USA Location/Qualifiers
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PRGTISKQDVCKTLCTRQPFSLAREACRSYSHVVLKEVRFFNLQVLYPLLSDPALNLR
IVHLVRDPRAVLRSREAAGPILARDNGIVLGTNGKWVEADPHLRLIREVCRSHVRIAE
AATLKPPPFLRGRYRLVRFEDLAREPLAEIRALYAFTGLTLTPQLEAWIHNITHGSGI
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 945
3 (bases 1 to 157337)
DOE Joint Genome Institute.

Direct Submission
Submitted (02-NOV-2001) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 945
On Nov 2, 2001 this Sequence version replaced gi:7689976.
Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality estimates above 40 are expected to have less than I error in 10,000 bp.
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All manually edited bases have been reduced to quality levels above 40 are expected to have less the error in 10,000 bp.
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5 DoE Joint Genome Institute.
5 Direct Submission
5 Submitted (OB-MAR-2000) Production Sequencing Facility,
6 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
2 (bases 1 to 194832)
5 DoE Joint Genome Institute and Stanford Human Genome Ce
5 Direct Submission
5 Submitted (21-DEC-2001) DOE Joint Genome Institute, 280
5 DoE Joint Genome Institute and Stanford Human Genome Ce
6 Direct Submission
7 Submitted (26-JAN-2002) DOE Joint Genome Institute, 280
8 Drive, Walnut Creek, CA 94598, USA
8 (bases 1 to 194832)
8 DOE Joint Genome Institute and Stanford Human Genome Ce
8 Direct Submission
8 Submitted (26-JAN-2002) DOE Joint Genome Institute, 280
8 Drive, Walnut Creek, CA 94598, USA
8 On Jan 26, 2002 this sequence version replaced gi:17976
8 Draft Sequence Produced by DOE Joint Genome Institute
8 Www.jgi.doe.gov
8 Finishing Completed at Stanford Human Genome Center
8 Www-shgc.stanford.edu
8 Quality: Phrap Quality >=40 99.4% of Sequence;
8 Estimated Total Number of Errors is 0.6.
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S DOE Joint Genome Institute.

Direct Submission
L Submitted (22-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 20, 2001 this sequence version replaced gi:7711893.

-----Genome Center
Center: Joint Genome Institute
"Anter Code: JGI
                                                                                                                                                                                                                                                                                                                                                                    Summary Statistics
Consensus quality: 140723 bases at least Q40
Consensus quality: 148960 bases at least Q30
Consensus quality: 151290 bases at least Q20
Consensus quality: 151290 bases at least Q20
Estimated insert size: 98000; pulse field gel estimation
Estimated insert size: 157572; sum-of-contigs estimation
Quality coverage: 7.39 in Q20 bases; pulse field gel estimation.

* NOTE: This is a 'working draft' sequence. It currently
consists of 16 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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Mammalia; Eutheria; Primates;
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DOE Joint Genome Institute.
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1 (bases 1 to 71503)

Akama, T.O., Nishida, K., Nakayama, J., Watanabe, H., Fujiwara, T., Nakamura, T., Maeda, N., Yamamoto, S., Nakamura, T., Dota, A., Kawasaki, S., Inoue, Y., Maeda, N., Yamamoto, S., Ozaki, K., Kinoshita, S., Shimomura, Y., Tanigami, A. and Fukuda, M.N. Macular corneal dystrophy type I and type II are caused by distinct mutations in a new sulphotransferase gene nutations in a new sulphotransferase gene Nat. Genet. 26 (2), 237-241 (2000)
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2 (bases 1 to 71503)
Akama, T.O. and Fukuda, M.N.
Direct Submission
Submitted (29-DEC-1999) Glycobiology Program, Th
Institute, 10901 North Torrey Pines Road, La Jol
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M Homo sapiens

Homo sapiens

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; HG

1 (bases 1 to 1462)

Lee,J.K., Bhakta,S., Rosen,S.D. and Hemmerich,S.

Cloning and characterization of a mammalian

N-acetylglucosamine-6-sulfotransferase that is highly x intestinal tissue

Biochem. Biophys. Res. Commun. 263 (2), 543-549 (1999)

99423499

2 (bases 1 to 1462)

Ee,J.K., Bhakta,S., Rosen,S.D. and Hemmerich,S.

Direct Submission

Submitted (10-AUG-1999) Respiratory Diseases, Roche Bic

Coration/Qualifiers

1. 1462

Ab_xref="taxon:9606"

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/db_x
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LAREACRSYSHVVLGADPHLRLIREVCRSHVRIAEAATLKPPPFLRGRYRLVRFED
LAREPLAEIRALYAFTGLTLTPQLEAWIHNITHGSGIGKPIEAFHTSSRNARNVSQAW
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Eukaryota; Metazoa; Chorua.

Bukaryota; Metazoa; Chorua.

Mammalia; Eutheria; Primates; Carua.

S. Hemmerich,S., Lee,J.K., Bhakta,S., Bistrup,A., Russen, S.D.

Chromosomal localization and genomic organization for thy galactose, N-acetylgalactosamine/N-acetylglucosamine

6-0-sulfotransferase gene family

NAL Glycobiology 11 (1), 75-87 (2001)

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INE 2 (bases 1 to 3786)

Hommerich,S., Bhakta,S., Lee,J.-K., Bistrup,A., Ruddle, Bosen,S.D.

LE Direct Submission

Bosen,S.D.

Location/Qualifiers

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2544)
Akama, T.O., Nishida, K., Nakayama, J., Watanabe, H., Fujiwara, T.,
Nakamura, T., Dota, A., Kawasaki, S., Inoue, Y., Maeda, N., Yamamoto, S.,
Ozaki, K., Kinoshita, S., Shimomura, Y., Tanigami, A. and Fukuda, M.N.
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/protein_id="AAG26325.1"
/db_xref="G1:11023146"
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DMDVFDAYLPWRRNLSDLFQWAVSRALCSPPACSAFPRGAISSEAVCRPLCARQSFTL
AREACRSYSHVVLKEVRFFNLQVLYPLLSDPALNLRIVHLVRDPRAVLRSREQTAKAL
AREACRSYSHVVLKEVRFFNLQVLYPLLSDPALNTRIVHLVRDPFLRGRYRLVRFEDL
AREDIAEIRALYAFTGLSLTPQLEAWIHNITHGSGPGARREAFKTSSRNALNVSQAWR
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/db_xref="taxon:9606"
/chromosome="16"
/map="16q22"
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/note="responsible for 693. .1880
/gene="CHST6"
/function="transfers sulfate"
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Consensus quality: 148960 bases at least 030
Consensus quality: 151290 bases at least 020
Estimated insert size: 98000; pulse field gel estimation
Estimated insert size: 157572; sum-of-contigs estimation
Quality coverage: 7.39 in 020 bases; pulse field gel estim
* NoTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
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Sequencing of Human Chromosome 5
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Direct Submission

Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US On Apr 25, 2001 this sequence version replaced gi:7689928.

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Center: Joint Genome Institute
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Sequencing of Human Chromosome 1
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Consensus quality: 180040 bases at least 040
Consensus quality: 192095 bases at least 030
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Estimated insert size: 195650; agarose-fp estimation
Estimated insert size: 206585; sum-of-contigs estimation
Quality coverage: 6.57 in 020 bases; agarose-fp estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 17 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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Lee, J.K., Bhakta, S., Rosen, S.D. and Hemme
Cloning and characterization of a mammali
N-acetylglucosamine-6-sulfotransferase th
intestinal tissue
Biochem. Biophys. Res. Commun. 263 (2), 5
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2 (bases 1 to 1989)
2 (bases 1 to 1989)
Lee, J.-K., Bhakta, S., Rosen, S.D. and Hemm
Direct Submission
Submitted (10-AUG-1999) Respiratory Disea
3401 Hillview Avenue, Palo Alto, CA 94304
Location/Qualifiers
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/codon_start=1
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Lee, J.K., Bhakta, S., Rosen, S.D. and Hemme
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N-acetylglucosamine-6-sulfotransferase th
intestinal tissue
Biochem. Biophys. Res. Commun. 263 (2), 5
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/map="8E1"
/tissue_type="intestine"
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/gene="I-GlcNAc-6-ST"
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/gene="I-GlcNAc-6-ST"
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QY	9	ccacctgcctcctgctcttcatcatctcccggccagggccctca
QQ	447	GATGGTACAGACTGGCATCCTGGTCTTCCTGGTCTCCCGGCAAGTGCCATCGTC
δŽ	320	ccagccggcggcgaggatcgtgtgcacgtgctggtgctgtcctcgtggcgctcgggctca 379
Dp	504	AGGCCTTGGGGAGCGTGTGCACGTGCTGGTACTGTCCTCGTGGCGCTCGGGCT
QY	380 564	tecttettgggecagetetteagecageacecegaegtettetaeetgatggagecegeg 439
QY	440	gtgtggaccaecetgtegeagggeagegegegeaaegetgeaeatggeettgege 49
qq	624	
Q.y Db	500	gacetgatgegetetatetttttgtgegacatggaegtgtttgatgeetacatgeeacag 559
٥٥	560	daaaacatatataaaataaaaaaaaaaaaaaaaaaaaaa
qq	744	TCTTCCAGIGGGCGGTGAGCCGCATIGIGCTCACTCCG 80
QY	620	ggcaccatcagcaagcaggacgtatgcaagacactgtgc 67
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Š	128U	cayctyctygyctaccyyctytytactctycyyaccaycaycytyacttcaccctyyat 1339

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## Wurny, D. M., Adams, C., Ado-Oduola, B., Ali-osman, F.R., Allen, C., Albrovoks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Banks, J., Bench, J., Baucharia, J., Bench, J., Suck, J., Banks, C., Harrell, K.L., Bardalh, D., Souck, J., Burkett, C., Harrell, K.L., Byd, N.C., Carron, T.P., Bubay, C., Burkett, C., Hurrell, K.L., Byd, N.C., Chen, G., Chondhry, I., Charket, D., Charket, D., Charket, C., Chordhry, I., Charled, J., Charled, M.C., Chon, T., Darbone, S.R., Chacko, J., Charled, M.C., Chon, T., Darbone, S.R., Darbin, M.C., Darbin, M.C., Darbone, S.R., Darbin, M.C., Edgar, D., Edwards, C., Elbaj, C., Elbaj, C., Edwards, M., Garcia, M., Haris, C., Harris, C., Harris, M., Harris, C., Harris, M., Karly, W., Martin, M., Martin, M.,
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of Medicine,
gi:15627284
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Worley, K.C.

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing

of Molecular and Human Genetics, Baylor College

of Molecular and Human Genetics, USA
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Dec 20, 2001 this sequence version replaced
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Rattus norvegicus clone C71 unordered pieces.
AC095664
AC095664.2 GI:17942230
HTG; HTGS_PHASE1.
Norway rat.
Rattus norvegicus
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Mammalia; Eutheria;
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Weinstock, G. and (
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model using sw - nucleic search, OM nucleic

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ALIGNMENTS

BE857538 7g0la08.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3305174 3' similar to TR:Q9UBY3 Q9UBY3 N-ACETYLGLUCOSAMINE 6-O-SULFOTRANSFERASE.;, mRNA sequence. BE857538 BE857538.1 GI:10371664 EST. Homo sapiens		cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov Seq primer: -40UP from Gibco High quality sequence stop: 431. Location/Qualifiers 1695 //Organism="Homo sapiens" //dL_xref="taxon:9606" //clone="IMAGE:3305174" //clone="IMAGE:3305174" //clone=lib="NCI_CGAP_Brn23" //tissue_type="glioblastoma (pooled)" //lab_host="DH10B"
RESULT 1 BE857538/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 735)

SOI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index

L Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
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Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CONA Library Arrayed by: Greg Lennon, Ph.D.

Cond distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINE, send email to: info@image.llnl.gov

Seq primer: -400P from Gibco

High quality sequence stop: 425.

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/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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1 (bases 1 to 525)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro-
Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Seq
Clone distribution: NCI-CGAP clone distribution inf
found through the I.M.A.G.E. Consortium/LLNL, send e
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human.

M Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae.

1 (bases 1 to 620)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAtional Cancer Institute, Cancer Genome Anatomy Profumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.I.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sec
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a No-oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and Fatima Bonaldo. "
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:2586803"
/clone=Lib="NCI_CGAP_CO20"
/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Normalized to Cot 500. Average insert size 1.11kb.
Normalized version of NCI_CGAP_Co18. Library constructed
by Life Technologies."
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project

Tumor Gene Index

Unpublished (1997)
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Functional annotation of a full-length mouse cDNA collection

Functional annotation of a full-length mouse cDNA collection

Functional annotation of a full-length mouse cDNA collection

B 5 (bases 1 to 1923)

S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Acno, H., Arai, A.,

Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,

Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,

Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F.,

Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Rasukawa, T.,

Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Roya, S.,

Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,

Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Shibata, K., Itoh, M., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Rashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Nakaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

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2 (sites)

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new gene Genome Res. 10 (10), 1617-1630 (2000)

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AK009113.1 GI:12843701
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) adult male tong clone_lib:RIKEN full-length enriched mouse cDN clone:2310003G18.

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertek Mammalia; Eutheria; Rodentia; Sciurognathi; Mus
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SOURCE

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Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shibata, Y., Shibata, K., Shibata, Y., Shibata, K., Shibata, Y., Sanawa, A., Takahashi, F., Tagawa, A., Tagawa, A., Takahashi, F., Tanaka, T., Tejama, Y., Toya, T., Yamamura, T., Yamanaka, T., Tanahaka, Y., Toya, T., Yamamura, T., Yamanaka, T., Tanahizaki, Y. Tayahizaki, Y. Sabhizaki, The Institute of Direct Submission of Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIXEN Tokohama Institute; 1-7-25 Subhizo-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama Institute; 1-7-25 Subhizo-cho, Tsurumi-ku, Yokohama, URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.go.jp/, Please visit our web site (http://genome.gsc.riken.go.jp/, Please visit our web site (http://genome.gsc.riken.go.jp/, Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 5.0 and subher adapter GAGAGAGAGATCATATAATAAATACCCCCCCCCC 3/). CDNA was cleaved with XDI and SSTI. Cloning sites, 5' end: XDI; 3' end: SSTI.
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/db_xref="MGD:MGI:1904558"
/db_xref="taxon:10090"
/clone="2310003G18"
/sex="male"
/tissue_type="tongue"
/clone_lib="RIKEN full-length enriched mouse cD/dev_stage="adult"
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Judie read and was generated as part of a large sequencing project of the Tetraodon nigroviridis www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers

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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ
This sequence is a single read and was generated
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Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertek
Actinopterygii; Neopterygii; Teleostei; Eutele
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontidae; Tetraodon.

1 (bases 1 to 1067)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fiz
Bouneau, L., Billault, A., Quetier, F., Saurin, W.
Weissenbach, J.
Charaterization and repeat analysis of the comfreshwater pufferfish Tetraodon nigroviridis
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/clone="033J20"
/clone_lib="G"
/note="Genoscope sequence ID : C
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S Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

L Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end """ and meay have higher chance of
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                                                                                    TCTTGGAGAACAGGCGCA---TGCCGGCCGCCGAGGTGCTGTATCAGGTCATGCAGGAGA
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Ag035205

AG035205

AG035205

AG035205.1 GI:16562078
GSS; GSS (genome survey sequence).

Pan troglodytes male lymphoblast DNA, clone—BAC Library clone:PTB-010M13.F.

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vert Mammalia; Eutheria; Primates; Catarrhini; Hc
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Fujiyama, A., Hattori, M., Toyoda, A.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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Bovine ESTs
Unpublished (2000)
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Gen University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Di 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
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placenta B
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                                  BAC
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                                                                            Score 322.8; DB 12
Pred. No. 7.3e-29;
; Mismatches 57;
                                  Male
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Eutheria; Cetartiodactyla;
Bovinae; Bos.
                                 a ee
/clone="PTB-010M13.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee
a 237 c 201 g 133
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BP250022A10E10 Soares r
clone BP250022A10E10 5'
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BF042384.1 GI:10759439
                                                                           Query Match
Best Local Similarity 86.0%;
Matches 382; Conservative
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| Mammalia; E
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PHRED
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/db_xref="taxon:9913"
/db_xref="taxon:9913"
/clone=lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
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from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP
This sequence is vector free and at least 200 bp in length.
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Pred. No. 3.8e-27;
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                                                FORWARD: TAATACGACTCACTATAGGG
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Moore, B.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murins

1 (bases 1 to 568)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Duk

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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   SW:C6ST_CHICK 092179 sequence.
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No. 1.2e-25;
                                                                                                                                                                                                                                                of MedicineP
                                                                                                                                                                                                                                                               st.
                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free th
IMAGE Consortium (info@image.llnl.gov)
MGI:969488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 295.4;
Pred. No. 1.2e
0; Mismatches
                                                                                                                                                                                  Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medivashington University School of Medivashington 286 1800
Tel: 314 286 1810
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Location/Qualifiers
1. .568
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IMAGE:1885164 5' similar t
6-SULFOTRANSFERASE;, mRNA
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Matches 381; Conser
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pCMV-SPORT6; Site_1: Not1; Site_2: ECORV (destroyed); RN
source anonymous pool of 6 male brains, age range 23-27;
male lung, age 27; and 1 male testis, age 69. Library i
oligo-dT primed and directionally cloned (ECORV site is
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                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information car

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11448 row: h column. 02
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Eukaryota; Metazoa; Chordata; Craniata; Vertek
Mammalia; Eutheria; Primates; Catarrhini; Homi
1 (bases 1 to 954)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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Como sapiens CDNA
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/db_xref="taxon:9606"
/clone="IMAGE:5179826"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled braipPCMV-SPORT6; Site_1: No+TSONT6;
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Score 284.2; Pred. No. 1.

13.98; 73.98;

Similarity

Match Local

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GSS; genome survey sequence.

Tetracdon nigroviridis.

SM Tetracdon nigroviridis.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;

Tetracdontidae; Tetracdon.

E 1 (bases 1 to 849)

S Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,

Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and

Weissenbach, J.

Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracdon nigroviridis

Unpublished
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ
This sequence is a single read and was generated
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Bernot, A., Fizames, C., Wincker, P., Brottier, P.,
Saurin, W. and Weissenbach, J.
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/db_xref="taxon:9606"
/clone="IMAGE:4385888"
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/tissue_type="lymphoma, cell line"
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Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                             linear EST 30-JAN-2 one IMAGE:4385888 5',
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Catarrhini;
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cDNA
                                             5 bp m
sapiens
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Pred. No. 1.4e
0; Mismatches
                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Straushr-
Email: cganhr
                                                                                                   Homo sapiens

Eukaryota; Metazoa; Chordata,

Mammalia; Eutheria; Primates

1 (bases 1 to 955)
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/sex- maie
//lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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                                                                                                                               TGGGGCGCACGGAGAAGCAGGTCCCTATATTGACCAAGGAGTTTGTGGTACGACCCTCCC
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0173108"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Rodentia; Sciurognat
1 (bases 1 to 433)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T
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84112, USA
Tel: 801 585
Fax: 801 585
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adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) and selected for ampicillin resistance."
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777	סי		97	4	-608-285A-5	equence 59, App
7 (9. 4.		35	m	-08-611-587-	aguence 1. Appl
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c 26	93.		\sim	N	-08-484-257-	equence 37 Appr
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-461-819-5 S94-08806-2 S95-01829-5 S95-16626-5 -646-301A-1 -481-968A-4 -154-712B-4	-08-724-394A- -08-724-394A- -08-724-394A-	-08-724-394A-2 -08-724-394A-2 -09-608-285A-5 -09-301-665-3	-09-078-29 -08-884-32 -08-975-08
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       US-09-045-284A-1
; Sequence 1, Application US/09045284A
; Patent No. 6265192
; GENERAL INFORMATION:
; APPLICANT: Bistrup, Annette
; APPLICANT: Rosen, Steven D.
; APPLICANT: Hemmerich, Stefan
; TITLE OF INVENTION: GLYCOSYL SULFOTRANSFERASE-3
; FILE REFERENCE: 6510-107US1
; CURRENT APPLICATION NUMBER: US/09/045,284A
; CURRENT FILING DATE: 1998-03-20
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 6.9e-69;
; Mismatches 360;
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645; Conser
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ORGANISM: Homo 8
09-045-284A-1
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Matches 645
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IBM PC compatible
YSTEM: PC-DOS/MS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                 Patent No. 5910581
GENERAL INFORMATION:
APPLICANT: HABUCHI,
APPLICANT: FUKUTA, N
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                  Sequence 1, Application Patent No. 5910581
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468;
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              34,115
R: TOYAM21.001AUS
             REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: TOY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714 760 9502
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2156
TYPE: nucleic acid
STRANDEDNESS: both
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est Local Similarity 54.0%;
atches 589; Conservative
                                                                                                                                     Fetal brain
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INFORMATION:
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LOCATION: 147..1583
IDENTIFICATION METHOD
S-08-899-514-1
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                                                                                          STRANDEDNESS: bor
TOPOLOGY: linear
MOLECULE TYPE: CDN
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ORGANISM: Humar
TISSUE TYPE: FF
        DANIEL
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
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APPLICATION NUMBER: US
FILING DATE: CONCURRENT
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US-09-009-656-11
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CITY: 1
STATE:
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CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION
AND TUMOR TREATMENT
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
HOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09009217; Patent No. 6132729; GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: Gao, Boning
TITLE OF INVENTION: CHEMOTHERAPEUT
TITLE OF INVENTION: CHEMOTHERAPEUT
TITLE OF INVENTION: AND TUMOR TRE?
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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P.O. Box 4433
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CLASSIFICATION:
IOR APPLICATION DATA:
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REGISTRATION NUMBER:
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Pred. No. 1.1e-31;
; Mismatches 98;
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Sequence 11, Application US/09009656

GENERAL INFORMATION:

APPLICANT: Thorpe, Philip E.

APPLICANT: King, Steven W.

APPLICANT: Gao, Boning

TITLE OF INVENTION: COMBINED TISSUE

TITLE OF INVENTION: METHODS AND CON

TITLE OF INVENTION: TREATMENT

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 SD:
    TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 13865 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Pred. No. 1.1e-31;
); Mismatches 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: AxyS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Ge
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inc
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
                                                                FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
                                                                                                      REFERENCE/DOCKET NUMBER: 41,071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR CT.
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US-09-009-913-1/c
; Sequence 1, Application US/0900991;
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: AxyS Pharmaceutical:
                                                                                                                                                                                                                                                        0;
                                                                                                                                                     INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 13865 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8744
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11 Similarity 73.7%;
278; Conservative
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S-09-009-656-11
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TATE:
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Pred. No. 9.6e-31;
); Mismatches 88;
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                                            Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91
                                                                                                                              NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows
                                            SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009, FILING DATE: 21-JAN-1998
CLASSIFICATION:
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ilarity 75.1%;
Conservative
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SEQUENCE CHARACTERISTICS:
LENGIH: 72928 base pairs
                                                                                                                                                                                                                                                      DNA
                                                                                                        Arraces:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                   Diskette
                                                                                                                                                                                                                                 double
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                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
         FORM
                                                                                                                                                                                                                          acid
                                                                                                                                                                                                                                             linear
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Best Local Similarity
Matches 268; Conser
ZIP: 94301
COMPUTER READABLE
MEDIUM TYPE: Di
                                                                                                                                                                                                                          nucleic
                                                                                                                                                                                                                                            TOPOLOGY: 1:
MOLECULE TYPE:
-09-009-913-1
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US-08-916-901-6
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SEE: Incyte Ph
: 3174 Porter
Palo Alto
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TOPOLOGY: linear
                                                                                                                  94304
           ADDRESSEE:
STREET: 31
CITY: Palc
STATE: CA
COUNTRY: U
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TITLE OF 1
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Best Local S
Matches 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 202.8; DB 2;
Pred. No. 8.7e-31;
; Mismatches 62;
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                                                                                                                                                                                           Version
                                                                                                    LISKETTE

COMPATIBLE

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Versi

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/916,901

FILING DATE: Filed Herewith

APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY / A COMPANIANCE CONTROLLY / A COMPANI
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US-09-154-602-6

Sequence 6, Application US/09154602

Patent No. 6300472

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Corley, Neil C.

APPLICANT: Shah, Purvi

TITLE OF INVENTION: RAB PROTEINS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Best Local Similarity 80.6%;
Matches 274; Conservative
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nucleic acid
DNESS: single
     П
                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
LENGTH: 2713 harr
     Porter
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TOPOLOGY: linear
 F: 3174 Por
Palo Alto
                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
-08-916-901-6
                                                              COUNTRY:
STREET:
CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 202.8; DB 4;
Pred. No. 8.7e-31;
; Mismatches 62;
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| GAGACTCCATCTCAAAAAAATAAATAAATAATTATGAA
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Inc
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Pharmaceutical
                                                                                                                                                                                                                                                     -0367
                                                                       DISKETTE

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows VE

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/00/1-
FILING DATE:
PRIOR APPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-395-800A-7

Sequence 7, Application US/08395800A

Patent No. 5807732

GENERAL INFORMATION:

APPLICANT: LOWE, JOHN B

APPLICANT: LENNON, GREGORY

APPLICANT: ROUQUIER, SYLVIE

APPLICANT: GIORGI, DOMINIQUE
                                                                                                                                                                                       08/916,901
                                                                                                                                                                                                                          NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T: LOWE, JOHN B
T: LENNON, GREGORY
T: ROUQUIER, SYLVIE
T: GIORGI, DOMINIQUE
T: KELLY, ROBERT J
INVENTION: GDP-L-FUCC
                                                                                                                                                                                                                                                                                                                                                                                                                     ch 9.9%; d Similarity 80.6%; 274; Conservative
                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
              H
                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pair
TYPE: nucleic acid
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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BETA-D-GALACTOSIDE

GDP-L-FUCOSE:

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R.; Mazuruk,
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sequence
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0
                                                                                                                                                                          MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
FORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
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ilarity 77.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      ERISTICS:
Base Pairs
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APPLICATION NUMBER: US/0
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
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                                                                                                               345 Park Avenue
                              Ignacio R.; Ma
Tombran-Tink,
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OTHER INFORMATION:
67-841A-43
                                                                              NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRES
ADDRESSEE: Morgan
                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader,
APPLICANT: Ignacio
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                                                                                                                         New York
New York
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TELEFAX: (2
INFORMATION FOR
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                                                                                                                       CITY: New Y STATE: New COUNTRY: US ZIP: 10154
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LOCATION:
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Pred. No. 1.4e-30;
); Mismatches 124;
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#
                                                                                                                                                         Version
                                                     OBLON, SPIVAK, MCCLELLAND, M. 55 S. JEFFERSON DAVIS HIGHWAY
                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,800A
FILING DATE: 28-FEB-1995
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -841A-43/c
e 43, Application US/08367841A
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703) 413-2220
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1 Similarity 69.7%;
287; Conservative
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nucleic acid
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INVENTION: 2-1
INVENTION: SAL
INVENTION: GE
OF SEQUENCES: 2
NDENCE ADDRESS:
                                                                                                      ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                    IBM PC
SYSTEM:
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TELEX: 248855 OP.
INFORMATION FOR SECTION
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ARLINGTON
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NUMBER OF SEQUEN
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                                                                                           COUNTRY: US
                                                     ADDRESSEE:
STREET: 17
                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
3-395-800A-7
                                                                                                                                    COMPUTER:
OPERATING
SOFTWARE:
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TYPE: n
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Best Local S
Matches 287
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PIGMENT EPITHELIUM
DERIVED FACTOR: CHARACTERIZATION
ORGANIZATION AND SEQUENCE OF THE
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Pred. No. 2.8e-30;
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for PEDF plus
Rodriguez,
, Krzysztof
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FP: 20264126US2
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                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264
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Pred. No. 3.4e-30;
; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09212971B

Patent No. 6107041

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G

APPLICANT: Mackenzie, Alexander E

APPLICANT: Baird, Stephen

APPLICANT: Baird, Stephen

APPLICANT: Bratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF IR

TITLE OF INVENTION: DETECTION AND MODULATION OF IR

TITLE OF INVENTION: DETECTION AND MODULATION OF IR

TITLE OF INVENTION: DATE: 1998-12-16

EARLIER APPLICATION NUMBER: 60/030,590

EARLIER APPLICATION NUMBER: 60/030,590

EARLIER APPLICATION NUMBER: 08/800,929

EARLIER FILING DATE: 1997-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FASLED FOR WINDOWS VERSION 4.0

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; LOCATION: (3677)...(39!
; OTHER INFORMATION: n c?
US-09-212-971-5
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Best Local
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PEDF GEN
                                                                                                                               RESULT 10
PCT-US95-07201-43/c
; Sequence 43, Application PC/TUS9507201
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, Sofia
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Patricia; Schwartz, Joan P.;
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PED
; TITLE OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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Pred. No. 2.8e-30;
); Mismatches 73;
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                                                                 1988
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FR: 20264126PCT
                                                                                                                                                                                                                                                                         STREET: 345 Park Avenue CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORDFELL
SOFTWARE: WORDFELL
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07201
                                                                            9541 CAAGACTCCATCTCAAAAAAAAAAAA
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FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: WORDPERFECT 5.1
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Best Local Similarity 77.6%;
Matches 256; Conservative
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) OTHER INFORMATION:
PCT-US95-07201-43
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                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US ZIP: 10154
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LOCATION:
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TREATMENT
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US-09-617-053A-5/c
; Sequence 5, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Frang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 3.4e
0; Mismatches
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (3677)...(3951)
OTHER INFORMATION: n can be a
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est Local Similarity 79.6%;
atches 249; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,929A

FILING DATE: 13-FEB-1997

CLASSIFICATION: 424
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26-APR-1996
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REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 078
                                                                                                                                                                                                      US/0880092
                                                                                                                                                                                                                                    Robert G
Alexande
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TELECOMMUNICATION INFORMATION
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
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Tsang, Benjamin F
Pratt, Christine
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CHARACTERISTICS:
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EDNESS: single
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Liston, Peter
Baird, Stephen
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & El
STREET: 176 Federal S
CITY: Boston
STATE: MA
COUNTRY: USA
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APPLICATION NUMBER:
FILING DATE: 14-NOV-
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US-08-800-929A-5/c; Sequence 5, Application U; Patent No. 6133437; GENERAL INFORMATION:
; APPLICANT: Korneluk,
; APPLICANT: MacKenzie,
                                                                                                                                                                                                                                   Korneluk,
                                                                                                                                                                                                                                                                                                OF INVENTION:
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MOLECULE TYPE:
8-800-929A-5
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Pred. No. 3.8e-30;
; Mismatches 42;
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R: M0828/7001
                                                                                                                                                                                           Munroe, David J.
Housman, David E.
ZENTION: AMPLIFICATION OF
                                                                                                                                                                                                                                                                                                                                                          MBER: US/08/133,629
07-0CT-1993
                                                                                                                                                                                                                                                                                 of America
                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                              8, Application US/08133629
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                                                                                                                                                                                                                                                                                                                                                                                                NAME: Greer, Helen
REGISTRATION NUMBER: 36,816
REFERENCE/DOCKET NUMBER: M082
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                          Wolf, Greenfield
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ilarity 82.5%;
Conservative
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LENGTH: 282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                      Massachusetts
X: United States
                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Munroe, David
APPLICANT: Housman, David
TITLE OF INVENTION: AMPI
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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FILING DATE: 07-0C
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STRANDEDNESS: sinc
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GENERAL INFORMATION:
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US-08-133-629-8
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JUS-09-608-285A-44/C

Sequence 42, Application US/09608285A

JEACHT N. Cold John

APPLICANT: Ford, John

APPLICANT: Ford, John

APPLICANT: Poug, George

TITLE OF INVENTION: METHODS AND MATERIALS REI

FILE REFERENCE: 28110/36570

CURRENT APPLICATION NUMBER: US/09/608,285A

CURRENT FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-07-16

PRIOR FILING DATE: 1999-03-19

PRIOR FILING DATE: 1999-03-19

PRIOR FILING DATE: 1999-02-04

PRIOR FILING DATE: 1998-07-16

PRIOR FILING DATE: 1998-07-16

PRIOR FILING DATE: 1998-07-16

PRIOR FILING DATE: 1998-07-08

PRIOR FILING DATE: 1998-07-08
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Human; glycosyl sulfotransferase-4alpha; GST-4alpha; immunosuppressive; therapy; selectin binding inhibitor; gene therapy; inflammation; systemic lupus erythematosus; SLE; rheumatoid arthritis; diabetes; polyarteritis nodosa; polymyositis; systemic sclerosis; dermatitis; glomerulonephritis; myasthenia gravis; Sjogren's syndrome; adrenalitis; Hashimoto's disease; Grave's disease; hypoparathyroidism; anaemia; demyelinating disease; cirrhosis; ulcerative colitis; allergic rhinitis; myocarditis; adult respiratory distress syndrome; eczema; psoriasis; asthma; hypersensitivity; rheumatic fever; tissue rejection; chromosome 16q23.1; ss.
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GST is a type 2 membrane protein useful for inhibiting a binding evel between a selectin and a selectin ligand, which comprises contacting selectin with a non-sulphated selectin ligand, GST and a small molecular that inhibits the sulphation activity of GST. GST is also useful inhibiting a selectin mediated binding event
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W hypotensive; dermatological; immunosuppressive; antidiabetic;
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W antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
W antionaemic; gene therapy; cancer; proliferative disorder; hypertension;
W neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
W cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
W cholesterol ester storage; systemic lupus erythematosus; infection;
W severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
W bone damage; cartilage damage; antiinflammatory disease; coagulation;
W thrombosis; contraceptive; ss. AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; vulnerary; cateopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antitinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antitihyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy concliberative disorders, neurodegenerative disorders, osteoarthritis, proliferative disorders, neurodegenerative disorders, severe condined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive. frame and peptides derived from open reading Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -NO:3421 П SEQ sednence 5507pp; English. polynucleotide \mathbf{BP} 2988 99US-0127607. 99US-0127636. 99US-0127728. 2000US-0540763. 2000WO-US08621 entry) CDNA; 2597-2599; Leach M; CURAGEN CORP (first 2000-602362/57. B; AAB41947. standard; ORF1711 WO200058473-A2. Page 31-MAR-1999; 02-APR-1999; 05-APR-1999; 30-MAR-2000; Homo sapiens 31-MAR-2000; RA, 08-FEB-2001 05-0CT-2000 Human ORFX AAC76156; AAC76156 Shimkets 5. P-PSDB; (CURA-) WPI

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CST is a type 2 membrane protein useful for inhibiting a binding event between a selectin and a selectin ligand, which comprises contacting the selectin with a non-sulphated selectin ligand, GST and a small molecular agent that inhibits the sulphation activity of GST. GST is also useful in inhibiting a selectin mediated binding event. GST is useful in gene therapy to treat disorders such as acute or chronic inflammation, systemic lupus erythematosus (SLE), rheumatoid arthritis, polyarteritis nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes, glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's disease, Grave's disease, adrenalitis, hypoparathyroidism, pernicious anaemia, demyelinating diseases, cirrhosis, ulcerative colitis, syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis, bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection, charing transplantation.
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Mouse; betal, 3GnT; betal, 3-N-acetylglucosaminyltransferase; MEC. L-selectin; L-selectin sulfotransferase-2; Crohn's disease; dialulcerative colitis; inflammatory skin disorder; psoriasis; Lichallergic contact dermatitis; lymphoma; chronic pneumonia; LSST-delayed-type hypersensitivity reaction; hyperplastic thymus; anantiinflammatory; antipsoriatic; antidiabetic; dermatological; antiallergic; intestinal-GlcNAc 6-sulfotransferase; I-GlcNAc6ST
        6-sulfotransferase
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Location/Qualifiers
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Hiraoka J, ž Fukuda

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OH comprises an expression of er ovary cells, Chinese hamster molecule, at directs that enzyme, useful for modifying acceptor ated L-selectin sulfotransferase-2 that ŗ. antigen, MECA-79 is 6-sulfotransferase ligand GlcNAc isolated L-L-selectin intestinal New

English 38pp; 10; Fig 26; Claim

യ don(colitis, t dermatitis, delayed-type us. This antagonist example by The of molecu Ör... CA-79 antigen expression f LSST-2 or its activated ing the expression treating L-selectin activity can be antigen. active fragment, where betal, 3GnT directs expression of a MECA-79 antige invention also provides a method of treating or preventing an L-selectin-mediated condition by reducing the expression or active betal, 3GnT that directs expression of a MECA-79 antigen. This can betal, 3GnT that directs expression of a MECA-79 antigen. This can by administering to the subject an oligosaccharide L-selectin ant that inhibits binding of L-selectin to a MECA-79 antigen, for exa administering antibody material that specifically binds betal, 3GnT antisense nucleic acid molecule. L-selectin sulforransferase-2 (LSST-2) also directs MECA-79 antigen expressificament can be reduced in combination with reducing the expressificactivity of betal, 3GnT. The mathod is actived. acceptor pneumonia, dastic thymus such as allergic contact mas, chronic pneumonia, d Crohn's disease and ulcerative ಡಿಗ diabetes and hyperplastic with reducing useful for trea modifying by contacting the acceptor with an isolated betal, 3-N-acetylglucosaminyltransferase (beffragment, where betal, 3GnT directs expression οĘ method encoding mouse e skin such lymphomas, The method ಹ invention provides the psoriasis and Lichen planus, hypersensitivity reactions, d such as itivity reactions, represents cDNA en ο£ disorders of betal,3GnT conditions su inflammatory present mediated seguence

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The present sequence is mouse glycosyl sulforransferase-4 (GST-4) cDNA.

GST-4 gene is found on chromosome BEI.

GST is a type 2 membrane protein useful for inhibiting a binding event

between a selectin and a selectin ligand, which comprises contacting the

selectin with a non-sulphation activity of GST is also useful

in inhibiting a selectin mediated binding event. GST is useful in gene

therapy to treat disorders such as acute or chronic inflammation,

therapy to treat disorders such as acute or chronic inflammation,

systemic lupus erythematosus (SLE), rheumatoid arthritis, polyarteritis

nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes,

glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's

disease, Grave's disease, adrenalitis, hypoparathyroidism, pernicious

anaemia, demyelinating diseases, cirrhosis, ulcerative colitis,

dermatitis, myocarditis, regional enteritis, adult respiratory distress

syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis,

bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection

during transplantation.
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3' ends of the cDNA consisted and nucleotide sequences of 5' and 3' ends of the cDNA construction of the protein encoded by construction of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length without any special methods. The present did not form part of the printed human cDNA of the invention.
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human; betal,3GnT; betal,3-N-acetylglucosaminyltransferase; MECA-79; ss;
L-selectin; L-selectin sulfotransferase-2; Crohn's disease; diabetes;
ulcerative colitis; inflammatory skin disorder; psoriasis; Lichen planus,
allergic contact dermatitis; lymphoma; chronic pneumonia; LSST-2;
delayed-type hypersensitivity reaction; hyperplastic thymus; antiulcer;
antiinflammatory; antipsoriatic; antidiabetic; dermatological;
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C Alternatively, the expression or activity of LSST-2 or its active fragment can be reduced in combination with reducing the expression or activity of betal, 3GnT. The method is useful for treating L-selectin mediated conditions such as Crohn's disease and ulcerative colitis, inflammatory disorders of the skin such as allergic contact dermatitis, psoriasis and Lichen planus, lymphomas, chronic pneumonia, delayed-type sequence represents cDNA encoding hyperplastic thurm.
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the invention. The nucleic acid sequences, probes and primers derived from these, proteins and antibodies are useful in detecting homologues. The sequences, antibodies and methods are useful in the diagnosis and treatment of diseases associated with selectin binding interactions, including conditions associated with or resulting from the homing of leukocytes to sites of inflammation and the normal homing of lymphocy
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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Note: The sequence data for this patent did not form part of th specification, but was obtained in CD-ROM format directly from
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The present sequence is human glycosyl sulfotransferase-4alpha (GST-4 alpha) cDNA. GST-4 gene is found on chromosome 16q23.1.

GST is a type 2 membrane protein useful for inhibiting a binding event selectin and a selectin ligand, which comprises contacting the between a selectin and selectin ligand, which comprises contacting the selectin with a non-sulphated selectin ligand, GST and a small molecular agent that inhibits the sulphation activity of GST is also useful in inhibiting a selectin mediated binding event. GST is useful in gene in inhibiting a selectin mediated binding event. GST is useful in gene therapy to treat disorders such as acute or chronic inflammation, systemic lupus erythematosus (SLE), rheumatoid arthritis, polyarteritis nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes, of systemic lupus arythenia gravis, Sjogren's syndrome, Hashimoto's disease, Grave's disease, adrenalitis, hypoparathyroidism, pernicious anaemia, demyelinating diseases, cirrhosis, ulcerative colitis, anyocarditis, regional enteritis, adult respiratory distress syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis, bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection
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The present sequence is human glycosyl sulfotransferase-4alpha (GST-4 alpha) cDNA. GST-4 gene is found on chromosome 16q23.1.

GST is a type 2 membrane protein useful for inhibiting a binding event cST is a type 2 membrane protein ligand, which comprises contacting the between a selectin and a selectin ligand, which comprises contacting the selectin with a non-sulphated selectin ligand, GST and a small molecular gent that inhibits the sulphation activity of GST. GST is also useful in inhibiting a selectin mediated binding event. GST is also useful in inhibiting a selectin mediated binding event. GST is also useful in inhibiting a selectin mediated binding architis, polyarteritis, condosa, polymyositis, dermatomyositis, rheumatoid arthritis, polyarteritis, glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's disease, Grave's disease, adrenalitis, hypoparathyroidism, pernicious dermatitis, myocarditis, regional enteritis, adult respiratory distress syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis, bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection during transplantation.
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; cantipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; cimmunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; cantidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating or the presence of or predisposition to, or preventing or treating nucleic acids can be used to express OREX proteins in gene therapy; concleic acids can be used to express OREX proteins in gene therapy; proliferative disorders, neurodegenerative disorders, osteoarthritis, proliferative disorders, neurodegenerative disorders, osteoarthritis, systemic lupus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
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GST is a type 2 membrane protein useful for inhibiting a binding event between a selectin and a selectin ligand, which comprises contacting the selectin with a non-sulphated selectin ligand, GST and a small molecular agent that inhibits the sulphation activity of GST. GST is also useful in inhibiting a selectin mediated binding event. GST is useful in gene therapy to treat disorders such as acute or chronic inflammation, systemic lupus erythematosus (SLE), rheumatoid arthritis, polyarteritis nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes, glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's disease, Grave's disease, adrenalitis, hypoparathyroidism, pernicious anaemia, demyelinating diseases, cirrhosis, ulcerative colitis, dermatitis, myocarditis, regional enteritis, adult respiratory distress syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis, bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection was a disingent and tissue rejection and tissue re

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The present sequence is human glycosyl sulfotransferase-4beta (GST-4 beta) cDNA. GST-4 gene is found on chromosome 16q23.1.
GST is a type 2 membrane protein useful for inhibiting a binding event between a selectin and a selectin ligand, which comprises contacting the selectin with a non-sulphated selectin ligand, GST and a small molecular agent that inhibits the sulphation activity of GST. GST is also useful in inhibiting a selectin mediated binding event. GST is useful in gene
                                                                                                                                                                                                                                    Human; glycosyl sulfotransferase-4beta; GST-4beta; immunosuppressive; therapy; selectin binding inhibitor; gene therapy; inflammation; systemic lupus erythematosus; SLE; rheumatoid arthritis; diabetes; polyarteritis nodosa; polymyositis; systemic sclerosis; dermatitis; glomerulonephritis; myasthenia gravis; Sjogren's syndrome; adrenalitis; Hashimoto's disease; Grave's disease; hypoparathyroidism; anaemia; demyelinating disease; cirrhosis; ulcerative colitis; allergic rhinitis myocarditis; adult respiratory distress syndrome; eczema; psoriasis; asthma; hypersensitivity; rheumatic fever; tissue rejection; asthma; hypersensitivity; ss.
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Human; drug metabolising enzyme; gene therapy; autoimmune disorder; inflammatory disorder; acquired immune deficiency syndrome; infection; AIDS; adult respiratory distress syndrome; cell proliferative disorder; allergy; anaemia; conjunctivitis; actinic keratosis; arteriosclerosis; cancer; endocrine disorder; hypothalamus disorder; pituitary disorder; gastrointestinal disorder; metabolic disorder; developmental disorder; liver disorder; iritis; cystic fibrosis; Addison's disease; retinitis; goitre; diabetes; dysphagia; gastric carcinoma; anorexia; eye disorder.

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Location/Qualifi

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of the invention are userul for assessing coxicity of test compounds and in gene therapy. Sequences of the invention are useful in the diagnosis, prevention and treatment of autoimmune/inflammatory of disorders such as acquired immune deficiency syndrome (AIDS), adult respiratory distress syndrome, allergies, anaemia, atherosclerosis, asthma, autoimmune haemolytic anaemia, contact dermatitis, Crohn's disease, flashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, psoriasis, systemic lupus erythematosus, rheumatoid arthritis, scleroderma, ulcerative colitis, uveitis, viral, bacterial, fungal, parasitic, protozoal, helminthic infections; cell proliferative disorders such as actinic keratosis, artherosclerosis, autherosclerosis, Duchenne and Becker dystrophy, hepatitis, Cushing's syndrome, cancers, myelodysplastic syndrome, epilepsy; endocrine disorders such as disorders of the hypothalamus and pituitary resulting from lesions such as primary brain tumours,
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The present sequence is mountained by the present sequence is mountained by the formulation useful for inhibiting a binding event serveen a selectin and a selectin ligand, which comprises contacting the between a selectin and a selectin ligand, which comprises contacting the selectin with a non-sulphated selectin ligand, GST and a small molecular gent that inhibits the sulphation activity of GST. GST is also useful in inhibiting a selectin mediated binding event. GST is useful in gene therapy to treat disorders such as acute or chronic inflammation, therapy to treat disorders such as acute or chronic inflammation, systemic lupus erythematosus (SLE), rheumatoid arthritis, polyarteritis, nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes, glomerulonephritis, myasthenia gravis, systemic sclerosis, diabetes, glomerulonephritis, myasthenia gravis, systemic sclerosis, diabetes, disease, darenalitis, hypoparathyroidism, pernicious anaemia, demyelinating diseases, cirrhosis, ulcerative colitis, dermatitis, myocarditis, regional enteritis, adult respiratory distress syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis, bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection during transplantation.
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Note: The sequence data for this patent did not form navt of the specification.
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                                                   This sequence encodes the human glycosyl sulfotransferase-3 (GST-3) the invention. The nucleic acid sequences, probes and primers derived from these, proteins and antibodies are useful in detecting homologues the sequences, antibodies and methods are useful in the diagnosis and treatment of diseases associated with selectin binding interactions, including conditions associated with or resulting from the homing of leukocytes to sites of inflammation and the normal homing of lymphocito secondary lymph organs.
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Human; betal, 3GnT; betal, 3~N-acetylglucosaminyltransferase; MECA-79; ss; L-selectin; L-selectin sulfotransferase-2; Crohn's disease; diabetes; ulcerative colitis; inflammatory skin disorder; psoriasis; Lichen planus, allergic contact dermatitis; lymphoma; chronic pneumonia; LSST-2; delayed-type hypersensitivity reaction; hyperplastic thymus; antiulcer; antiinflammatory; antipsoriatic; antidiabetic; dermatological;
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by contacting the acceptor with an isolated
betal,3-N-acetylglucosaminyltransferase (betal,3GnT) or an
fragment, where betal,3GnT directs expression of a MECA-79
invention also provides a method of treating or preventing
L-selectin-mediated condition by reducing the expression or
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betal, 3GnT that directs expression of a MECA-79 antigen. This can be administering to the subject an oligosaccharide L-selectin antage that inhibits binding of L-selectin to a MECA-79 antigen, for examply administering antibody material that specifically binds betal, 3GnT, and/or a betal, 3GnT antisense nucleic acid molecule. L-selectin and/or a betal, 3GnT antisense nucleic acid molecule. L-selectin sulfotransferase-2 (LSST-2) also directs MECA-79 antigen expression sulfotrantively, the expression or activity of LSST-2 or its active fragment can be reduced in combination with reducing the expression activity of betal, 3GnT. The method is useful for treating L-selectin mediated conditions such as Crohn's disease and ulcerative colitis, inflammatory disorders of the skin such as allergic contact dermating psoriasis and Lichen planus, lymphomas, chronic pneumonia, delayed-humaniatismit.
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
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Note: The sequence data for this patent did not form part of the printe specification, but was obtained in CD-ROM format directly from EPO.
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; CURRENT FILING DATE: 1998-03-20
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGIH: 2032
; TYPE: DNA
; ORGANISM: Homo sapiens
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FOR THE POLYPEPTIDE
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DRIVE, SIXTEENTH FL
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NEWPORT BEACH
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YSTEM: PC-DOS/MS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy
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GENERAL INFORMATION:
APPLICANT: HABUCHI, C APPLICANT: FUKUTA, MA TITLE OF INVENTION: E TITLE OF INVENTION: E
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                REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: TOYAM21.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714 760 0404
TELEFAX: 714 760 9502
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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IDENTIFICATION METHOD:
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ORIGINAL SOURCE:
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STRANDEDNESS:
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US/08/655,878
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HABUCHI, OSAMI
VENTION: DNA CODING FOR
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US-08-655-878-1
; Sequence 1, Application US/08655878
; Patent No. 5827713
; GENERAL INFORMATION:
; APPLICANT: FUKUTA, MASAKAZU
; APPLICANT: HABUCHI, OSAMI
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IBM PC compatible
YSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TRNGTH: 2354
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CORRESPONDENCE ADDRESS:
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STATE:
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SOFTWARE: Patentin
CURRENT APPLICATION DATA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LOCATION: 394..402
IDENTIFICATION METHOD: S
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LOCATION: 427..435
IDENTIFICATION METHOD: S
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LOCATION: 1537..1545
IDENTIFICATION METHOD: S
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LOCATION: 280..321
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LOCATION: 1405..1413
IDENTIFICATION METHOD: S
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LOCATION: 916..924
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LOCATION: 211..309
IDENTIFICATION METHOD:
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LOCATION: 310..1584
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TITLE OF INVENTION: POLYPEPTIDE OF N-ACETYLGLUCOSAMINE-6
TITLE OF INVENTION: DNA ENCODING THE SAME
FILE REFERENCE: TOYAM41.001AUS
CURRENT APPLICATION NUMBER: US/09/263,023
CURRENT FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: JP 10-54007
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Sequence 3, Application US/0926302
Patent No. 6037159
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GENERAL INFORMATION:
APPLICANT: Uchimura, Kenji
APPLICANT: Kadomatsu, Kenji
APPLICANT: Kannagi, Reiji
APPLICANT: Habuchi, Osami
APPLICANT: Muramatsu, Takashi
TITLE OF INVENTION: POLYPEPTIE
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R FILING DATE: 1998-03-05
R APPLICATION NUMBER: JP 10-1
R FILING DATE: 1998-06-24
OF SEQ ID NOS: 10
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SOFTWARE: FastSEQ f
SEQ ID NO 3
LENGTH: 2409
TYPE: DNA
ORGANISM: HOMO SAP.
FEATURE:
NAME/KEY: CDS
LOCATION: (390)...
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LILLY CORPORATE CENTER
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Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
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NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
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LENGTH: 43280 base par
TYPE: nucleic acid
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MOLECULE TYPE
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LOCATION:
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ZIP: 462
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CITY: I
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Sequence 1, Application US/09263023;
Patent No. 6037159;
GENERAL INFORMATION:
APPLICANT: Uchimura, Kenji
APPLICANT: Kanomatsu, Hideki
APPLICANT: Kanomatsu, Reiji
APPLICANT: Kanomagi, Reiji
APPLICANT: Habuchi, Osami
APPLICANT: Habuchi, Osami
APPLICANT: Habuchi, Osami
APPLICANT: TILE OF INVENTION: POLYPEPTIDE OF N-ACETY
TITLE OF INVENTION: DNA ENCODING THE SAME
FILLE REFERENCE: TOYAM41.001AUS
CURRENT APPLICATION NUMBER: US/09/263,023
CURRENT FILING DATE: 1998-03-05
EARLIER APPLICATION NUMBER: JP 10-177844
BARLIER FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 3.0
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Pred. No. 1
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    Sequence 63, Application US/09040984
    Patent No. 6210883
    GENERAL INFORMATION:
        APPLICANT: Reed, Steven G.
    APPLICANT: Wang, TongTong
    TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
                                                                                                                                                                                                                                 Score 64.6; D. Pred. No. 4.8e 0; Mismatches
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Pred. No. 0.00068;
; Mismatches 72;
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APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR FILE REFERENCE: 210121.455c1
CURRENT APPLICATION NUMBER: US/09/123,912A; CURRENT FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: 09/040,802
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
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NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.456

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

TELEPHONE: 206-282-6031
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Local Similarity 58.48;
les 101; Conservative
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NAME: Maki, David J.
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PatentIn V
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Patent No. 5589385
GENERAL INFORMATION:
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Cyanamid Plaza
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NAME/KEY: modified_
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Cloning of the bios
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle J
TON NUMBER: 31,145
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                                                                APPLICATION NUMBER: US/08/125,468 FILING DATE: 22-SEP-1993
           IBM PC compatible YSTEM: PC-DOS/MS-DOS PatentIn Release #1.0,
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Patent No. 5866410
GENERAL INFORMATION:
APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of t.
TITLE OF INVENTION: useful there
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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3 Plaza
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REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
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Pred. No. 0.0016;
0; Mismatches 173;
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APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expr
TITLE OF INVENTION: From Multiple Transfected Ep
FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
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                                                                                                                                                                 NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,255-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3241
TELEFAX: (201)831-3305
                                                                                       US/08/474,933
                                                    Release #1.0,
                                                                                                                                      46
                                                                                                                                  APPLICATION NUMBER: US 08/125
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
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5. 5976807
                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: Patentin Release:
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                                Floppy disk
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Local Similarity 48.28;
les 161; Conservative
                                                            SOFTWARE: Patentin Re
CURRENT APPLICATION DATA
APPLICATION NUMBER: U
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COUNTRY: USA
ZIP: 07470
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TOPOLOGX: linear
                                                                                                            CLASSIFICATION:
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Patent No. 5976807
GENERAL INFORMATION:
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                                                                                                FILING DATE:
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
TITLE OF INVENTION: DNA encoding methymycin an FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A; CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43; SOFTWARE: FastSEQ for Windows Version 3.0
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Windows Version
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Local Similarity 44.7%;
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Query Match
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Matches 225; Conser
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Patent No. 6117659
GENERAL INFORMATION:
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FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105
CURRENT FILING DATE: 1998-06-26
CURRENT FILING DATE: 1998-06-26
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Patent No. 6265202
GENERAL INFORMATION:
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 Local Similarity
es 225; Conser
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SOFTWARE: FastSEQ
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APPLICANT: MCDANIEL, F
APPLICANT: TANG, Li
TITLE OF INVENTION: RF
FILE REFERENCE: 300622
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Va
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APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mamma
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

protein search, using sw model OM protein

20, 2002, 19:58:31 September Run on:

; Search time 13.53 Seconds
(without alignments)
1116.085 Million cell updates/sec

....LTLDLYLPRGPDHFSWASPD US-09~593-828-8 2051 1 MWLPRFSSKTVTVLLLAQTT.. Title: Perfect score: Sequence:

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105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

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Gaps 31; Length 458; Indels Query Match Best Local Similarity 34.3%; Pred. No. 2.2e-41; Matches 124; Conservative 66; Mismatches 141;

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                                                                                           -POSRNLSAFFNWATSRALCSPPACSAFPRGTISKQD
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FUNCTION: CATALYZES THE O-SULFATION OF TYROSINE RESIDUES VACIDIC MOTIFS OF POLYPEPTIDES (BY SIMILARITY).

CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + protein tyansine 3',5'-bisphosphate + protein tyrosine-O-sulfate subcellular Location: Type II membrane protein. Golgi memb similarity).

SIMILARITY: BELONGS TO THE PROTEIN SULFOTRANSFERASE FAMIL:
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Putative protein-tyrosine sulfotransferase (EC
(Tyrosylprotein sulfotransferase) (TPST).
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Rhabditidae; Peloderinae; Caenorhabditis
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WormPep; F42G9.8; CE07235.
InterPro; IPR000863; Sulfotransferase
Pfam; PF00685; Sulfotransfer; 1.
Hypothetical protein; Transferase; Tra
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Haft D., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Spelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and "Whole genome comparison of Mycobacterium tuberculosis clinical and "Whole genome comparison of Mycobacterium tuberculosis
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harricole S.T., Brosch R., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroycoliver S., Devlin K., Krogh A., McLean J., Moule S., Murphy L., Cliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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l kDa protein Rv2267c.
9 OR MTCY339.43.
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Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; NCBI_TaxID=1773;
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                                                   the burched by non-profit institutions as long as its contains to commercate by and for commercatified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.isb-sib.ch/announor send an email to license@isb-sib.ch).
                             tht. It is produced through a collabora Bioinformatics and the EMBL cutstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEX CATALYZES THE OVERALL & CO(2). IT CONTAINS MULTIPLE: PYRUVATE DEHYDROGENASE (E1), 52) & LIPOAMIDE DEHYDROGENASE
                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                                                                                                     \infty
                                                                                                                                                                                                                                                                                                                                                         \mathbf{\omega}
                                                                                                                                                                                                                                                                                                                                                                            243
                                                                                                                                                                                                                                                                                                                                                                                               284
                                                                                                                                                                                                                                     Gaps
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alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      testis-specific type II).
                                                                                                                                                                                                                                                                                        MAVRDLMRSIFLCDMDVFDAYMPQSRNLSAFFNWATSRALCSPPACSAFPRGTISKQDVC
                                                                                                                                                                                                                                                     -PDVFYLMEPAWHVWTTLSQGSAATLH
                                                                                                                                                                                                                                                                           -WEAPYVEFLVSKH
                                                                                                                                                                                                                                                                                                                                                                           -GINGKWVEADPHLRLI
                                                                                                                                                                                                                                                                                                                                                                                  VLLEVFPQAKFIHIVRDPYVVYPSTIHLHKALYRIHGLQQPTFDGLDDKVVST--YVDLY
                                                                                                                                                                                                                                                                                                                                                 -NRPPQYEEYLDLEQVAPRELE--IWKRTLFRFVQQVYFRRKTVILKNPTHSFRIK
                                                                                                                                                                                                                                                                                                                                     -PLLSDPALNLRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi
                                                                                                                                                                                                                                   89;
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chromosome 4.";
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G
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                                                                                                                                                                                                                                                                                                                                                                                                                                    324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subunit is coded for by an intronless gene on chromosome 4. Genomics 8:225-232(1990).

-!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES

CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brown
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                                                                                                                                                                                                                                                                                                                                                                                                                         REVCRSHVRIAEAATLKPPPFLRGRYRLVRFEDLAREPLAEIRALYAFTGL
            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                         · | | : | | | : | | | | - | HPQEDE----FVWC-MQGLPSPYLTIAFP
                                                                                                                                                                                   CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha subunit, t
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                                                                                                                                    TubercuList; Rv2267c; -.
InterPro; IPR000863; Sulfotransferase.
Pfam; PF00685; Sulfotransfer; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 388 AA; 46062 MW; 5DED0263275A9B24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=2249846;
n R.M., Hutchison W.M., Maragos
c form of the human pyruvate del
                                                                                                                                                                                                                                                             \Omega
                                                                                                                                                                                                                                                                                                                                                                       -VHLVRDPRAVLRSREAAGPILARDNGIVL --
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                                                                                                                                                                                                             Score 102.5; DB Pred. No. 0.091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 25, Created)
93 (Rel. 25, Last sequence update)
701 (Rel. 40, Last annotation update)
dehydrogenase El component alpha sub
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                           SWISS-PROT entry is copyright. It is sen the Swiss Institute of Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Ve
Catarrhini;
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ursor (EC 1.
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                                                                                                                                                                                                                               37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                                                                                                         Z77163; CAB00968.1; -
AE007076; AAK46611.1;
                                                                                                                                                                                                            Similarity 22.7%; 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               -KLDEGRELVDPT--
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                                                                                                                                                                                                                                                 VLVLSSWRSGSSFLGQLF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
  r strains.";
(APR-2001)
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                             MT2329;
                                                  European
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P29803;
01-APR-1993
01-APR-1993
16-OCT-2001
  aboratory
 laboratory
Submitted
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                                      between
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PDHA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ~
                                                                                                                                           SPERMATOGENI
                                                                                                                                                                                                                                                                                                                                                                   MIM; 179061; -.

InterPro; IPR001017; El_dh.

Pfam; PF00676; El_dehydrog; 1.

Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;

MICOCHONDRION (BY SIMILARITY).

TRANSIT 1 27 MITOCHONDRION (BY SIMILARITY).

TRANSIT 1 27 MITOCHONDRION (BY SIMILARITY).

THANSIT 1 27 MITOCHONDRION (BY SIMILARITY).

MOD_RES 230 230 PHOSPHORYLATION (BY SIMILARITY).

THOO_RES 291 291 PHOSPHORYLATION (BY SIMILARITY).

THOO_RES 298 298 PHOSPHORYLATION (BY SIMILARITY).

THOO_RES 298 298 PHOSPHORYLATION (BY SIMILARITY).
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                                                PHOSPHORYLATION N) OF THE ALPHA
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eudicots;
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                                                                                                      SUBUNITS
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                                                                  (ACTIVATION)
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                                                BY
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core
Asteridae; euasterids I; Solanales; Convolvulaceae;
                                                                                                    BETA
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                                                REGULATED
                                                                                           SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BET, SUBCELLULAR LOCATION: Mitochondrial matrix TISSUE SPECIFICITY: TESTIS. EXPRESSED IN PUBLIS.
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Pred. No. 0.35;
25; Mismatches
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.5).
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acetyldihydrolipoamide + CO(2).
COFACTOR: THIAMINE PYROPHOSPHATE.
ENZYME REGULATION: E1 ACTIVITY IS REG
(INACTIVATION) AND DEPHOSPHORYLATION
SUBUNIT.
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Last sequence up
Last annotation
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ILQDRM-
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Rel. 13,
Rel. 40,
ammonia-
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DAAQFATTDPEPHL
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(Rel. 13
(Rel. 40
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P14166;
01-JAN-1990 (R
01-JAN-1990 (R
16-OCT-2001 (R
Phenylalanine a
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Tanaka Y., Mat
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MIM; 179061;
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Odontella sinensis.
Plant Mol. Biol. Rep
-!- FUNCTION: MAY II
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P23052;
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Best Local S
Matches 89
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VGLP_BEV
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                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                it institutions as long as its content is in no ways statement is not removed. Usage by and for commercials a license agreement (See http://www.isb-sib.ch/announce/to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                          MODIFIED TO FORM 4-METHYLIDENE-IMIDAZOLE 5-ONE (BY SIMILARITY). 87B9513A91228FBB CRC64;
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                                 国园
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                                                                       PATHWAY: KEY ENZYME OF PHENYLLFROFANCLE ....
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
PTM: CONTAINS AN ACTIVE SITE 4-METHYLIDENE-IMIDAZOLE-5-ONE (MIO)
                                 ΠH
                                           WID
                                                     SKELETON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -VRFFNLOVLYPLLS---DPALNLRIVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SRSGRRIFRVASPR
  phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -FTGLTLTPQLE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Freier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ceae;
                                                                                                                                                                                                                                                                                                                                                                                                                     FGNATESCHTLPHSATRAAMLVRINTLLQGYSGIRFEILEAITKLLNHNITPCLPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                               LVRDPRAVLRSREAAGPILARDNGIVLGTNGKWVEADPHLRLIREVCRSHVRIAEAA
                                                                                                                                                                                                                                                                                                                                                                                  58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clpA homolog
                                                                +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coscinodiscophy
ceae; Odontella
                                                     VARIETY OF NATURAL PRODUCTS BASED ON THE PHENYLPROPANE CATALYTIC ACTIVITY: L-phenylalanine = trans-cinnamate + PATHWAY: KEY ENZYME OF PHENYLPROPANOID METABOLISM.
                                                                                                                                                                                                                                                                                                                                                            Length 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a chlorophyll a+c-conts:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                         WHICH IS FORMED AUTOCATALYTICALLY BY CYCLIZATION OF RESIDUES ALA-SER-GLY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE PAL / HISTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TSSRNARNVSQAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQIEAAAIMEHILDGSSYVKAAQKLHEMDPLQKPKQDRYALRTSPQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; stramenopiles; Bacillariophyta; Coscil
Biddulphiophycidae; Eupodiscales; Eupodiscaceae;
NCBI_TaxID=2839;
                                                                                                                                                                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          : :: || | | : | || : || || : || || TIASGDLVPLSYIAGLITGRPNSKAVGPNGETLNAEEALRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
It clp protease ATP-binding subunit
                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                      PAL_HISTIDASE; 1.
anoid metabolism; Multigene
                                                                                                                                                                                                                                                                                                                                                                     0.77;
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                                                                                                                                                                                                                                                                                                                                                            Score 96;
Pred. No.
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Kowallik K.V., Stoebe B., Schaffran
"The chloroplast genome of a chlorop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AWIHNITHGSGIGKPIEAFH-
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                                                                                                                                                                                                                                                                                                                                77138 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                               Phenylpropanoid 192 194
                                                                                                                                                                                                                                                S29029.
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Best Local Similarity
' * ~ hes 57; Conserva
                                                                                                                                                                                 use by non-profit modified and this stentities requires a
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01-FEB-1996
16-OCT-2001
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P49574;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                       ΝI
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                       PROTEASE INVOLVED S CHLOROPLAST.
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J. Repeat; Chloroplast.

ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).

ATP (POTENTIAL).
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t Mol. Biol. Rep. 13:336-342(1995).

FUNCTION: MAY INTERACT WITH A CLPP-LIKE PRODEGRADATION OF DENATURED PROTEINS IN THE CHISUBCELLULAR LOCATION: Chloroplast.

SIMILARITY: BELONGS TO THE CLPA/CLPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ĥ
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Pred. No. 1.3;
9; Mismatches
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-GKTAVAEGLAQLI
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                                                                                                                                                                                                                                                                                               EMBL; Z67753; CAA91619.1; -.
InterPro; IPR003593; AAA.
InterPro; IPR003959; AAA_subfam.
InterPro; IPR001270; CLP_AB.
InterPro; IPR004176; Clp_N.
                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00004; AAA; 1.

Pfam; PF02861; Clp_N; 2.

PRINTS; PR00300; CLPPROTEASEA.

SMART; SM00382; AAA; 1.

PROSITE; PS00870; CLPAB_1; 1.

PROSITE; PS00871; CLPAB_2; 1.

Chaperone; ATP-binding; Repeat;

NP_BIND 218 225 ATP

NP_BIND 560 567 ATP

SEQUENCE 885 AA; 99917 MW;
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                                                          Nidovirales;
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of the Berne
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                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1581
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                            OF
                                                                                                                                                          EDIATES THE BINDING OF INVOLVED IN MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNWATSRALCSPPACSAFPRGTISKQDVCKTLCTRQPFSLAREACRSYSHVV
                                                                  NCBL_TaxID=11120,

[1]
SEQUENCE FROM N.A.
STRAIN=ISOLATE P138/72;
MEDLINE=91020973; PubMed=2219698;
Anijder E.J., den Boon J.A., Spaan W.J.M., Weiss M., Hor "Primary structure and post-translational processing of virus peplomer protein.";
I virus peplomer protein.";
L virology 178:355-363(1990).
--- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING CONTROLOGY 178:355-363(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                         stage;
                                                                                                                                                                                                                                                                               Signal
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                                                                                                                                                                                                                                                                          Glycoprotein; Envelope protein; Transmembrane; SIGNAL 1 19
           Last sequence update)
Last annotation update)
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418
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Mismatches
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                                                    Viruses; ssRNA positive-strand viruses,
Coronaviridae; Torovirus.
NCBL_TaxID=11156;
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N-LINKED (
MW; 00D91E
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ilarity 17.6%;
Conservative 6
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A36759; VGWJBV.
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CARBOHYD
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Best Local S
Matches 81
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in no way commercial
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in sulfotransferase homologue
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e-O-sulfate.
. Golgi membrane (
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ROSINE RESIDUES WITHIN
       -ILARDNGIVLGTNGKWVEADPHLRLIREVCRSHVRIAEAATLKP
                                                                                                                                                                                                              HP--AGVIMIARHHSMWSVAARNSTSFYCVTHSLTTFGKLDISTSWFFHTLALPSGPVSQ
                                                                                                                                                                                                                                                                                                      -HGSGIGKPIEAFHTSSRNARNVS
                                                                                                                                                                                                                                                                                                                                                                     -TLTTQLQAYAQVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
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FUNCTION: CATALYZES THE O-SULFATION OF TYROSINE RESIDUES W.
ACIDIC MOTIFS OF POLYPEPTIDES.
CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + protein typadenosine 3',5'-bisphosphate + protein tyrosine-O-sulfate.
SUBCELLULAR LOCATION: Type II membrane protein. Golgi membranilarity).
SIMILARITY: BELONGS TO THE PROTEIN SULFOTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
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CYTOPLASMIC (POTENTIAL).
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on update)
(EC 2.8.2.20)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              371
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                                           QAWRHALPFTKILRVQEVCAGALQLLGYRPVYSADQQRDL
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380
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EMBL; AL132904; CAC35844.1; -..
WormPep; Y111B2A.15; CE26632.
InterPro; IPR000863; Sulfotransferase.
Pfam; PF00685; Sulfotransfer; 1.
                                                                                                                                            PPFLRGRYRLVRFEDLAREPLAEIRALYAFT
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273:24770-24774(1998)
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence
16-OCT-2001 (Rel. 40, Last annotation
Protein-tyrosine sulfotransferase A
sulfotransferase-A) (TPST-A).
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Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    t
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STRAIN-BRISTOL N2;
Sulston J.E.;
Submitted (MAR-2000) t
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N2;
         -RSREAAGP
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALL BOUND TO THE PROTEIN (BY SIMILARITY).

SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                            GRYRLVRFEDLAREPLAEIRALYAFTGLTLTPQLEAWIHNITHGSGIGKPIEAFHTSSRN
                                                                                                                                                      -FYLMEPAW----HVWTTLSQG--SAATLHMAV
                                                                                                                                                                                                           RDLMRSIFLCDMDVFDAYMPQSRNLSAFFNWATSRALCSPPACSAFPRGTISKQDVCKTL
                                                                                                                                                                                                                                                               CTROPFSLAREACRSYSHVVLKEVRFFNLQVLYPLLSDPALNLRIVHLVRDPRAVLRSRE
                                                                                                                                                                                                                                                                                                                     AAGPILARD ---NGIVLG ----TNGKWVEADPHLRLIREVCRSHVRIAEAATLKPPPFLR
                                                                                                                                                                                                                                                                                                                                                                                                      --VYYEQLVLHPEAQMRRITEFLDI---PWDDKVLH---HEQLIGKDISLSNVERSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi; erpentes; Colubroidea;
                                                                                                                                                                     -VGHGDRAPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=20229584; PubMed=10764543;
Slowinski J.B., Keogh J.S.;
"Phylogenetic relationships of elapid snakes based on cytochrome
                                                                                                                                                                                                                                                                                          --NAKYLLMIRDGRATVNS-
             (POTENTIAL).
LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
FF709BF00F1EDC95 CRC64;
SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                               -IISRKVTITGFDLNDFRQCMTKWNAA---IQIMVDQCES---VGEKNCLK-
                                                                                              Length 380;
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   361
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Serpentes;
                                                                                                                           108;
                                                                                              DB 1;
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                                                                                             Score 90.5; D'
Pred. No. 1.1;
3; Mismatches
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Lepidosauria; Squamata; Scleroglossa;
Elapidae; Laticaudinae; Laticauda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 40, Created)
(Rel. 40, Last sequence ug
(Rel. 40, Last annotation
                                                                                                                          43;
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43
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                                                          AA;
                                                                                                              Similarity
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Phylogenet.
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Mitochondrion.
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16-0CT-2001
16-0CT-2001
16-0CT-2001
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Best Local S
Matches 66
                                           CARBOHYD
SEQUENCE
    TRANSMEM
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STRAIN=CIAT899;
MEDLINE=97002746; PubMed=8850086;
Folch-Mallol J.L., Marroqui S., Sousa C., Manyani H van der Drift K.M.G.M., Haverkamp J., Quinto C., Gi Thomas-Oates J., Spaink H.P., Megias M.;
"Characterization of Rhizobium tropici CIAT899 nodu role of nodH and nodPQ genes in their sulfation.";
Mol. Plant Microbe Interact. 9:151-163(1996).
-:- FUNCTION: REQUIRED FOR THE FORMATION OF SULFATE PROPOSED TO TRANSFER ACTIVATED SULFATE (PAPS) T
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STRAIN=CFN 299;
MEDLINE=96303535; PubMed=8755625;
Laeremans T., Caluwaerts I., Verreth C., Rogel M.A Vanderleyden J., Martinez-Romero E.;
"Isolation and characterization of Rhizobium tropic sulfation genes.";
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                                              EMBL; AF217834; AAF37253.1; -.
InterPro; IPR000179; Cyt_b_b6.
Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
PROSITE; PS00193; CYTOCHROME_B_QO; 1.
PROSITE; PS00192; CYTOCHROME_B_HEME; F
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Rhizobiaceae; Rhizobium.
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                                            restrictions
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J. Biol. Chem. 273:24770-24774(1998).

-!- FUNCTION: CATALYZES THE O-SULFATION OF TYROSINE RESIDUES WITHIN ACIDIC MOTIFS OF POLYPEPTIDES.

-!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + protein tyrosine-0-sulfate.

adenosine 3',5'-bisphosphate + protein tyrosine-0-sulfate.

-!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse tyrosylprotein
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               This SWISS-PROT entry is copyright. It is predetween the Swiss Institute of Bioinformatithe European Bioinformatics Institute. There use by non-profit institutions as long amodified and this statement is not removed. entities requires a license agreement (See For send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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X87608; CAA60912.1;
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SIGNAL-ANCHOR (TYPE-II MEMBRANE FROL.)

LUMENAL, CATALYTIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -FYLMEPAWHVWTTLSQGSAATLHMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dohrmann
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Homo
 SULFOTRANSFERASE
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                                                                                                                                                                                                                            Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                   112;
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on update)
(EC 2.8.2.2
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 86.5; DB Pred. No. 2.5; 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF049890; AAC36060.1; -.
MGI:1309516; Tpst2.
Pro; IPR000863; Sulfotransferase.
PF00685; Sulfotransfer; 1.
sferase; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND TISSUE SPECIFICITY MEDLINE=98409623; PubMed=9736702; Beisswanger R., Corbeil D., Vannier C., The Folling R., Niehrs C., Huttner I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Ve
Catarrhini;
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PROTEIN
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342
367
42067 MW;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                    4.2%;
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BELONGS
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Pfam; PF00685;
                                                                                                                                                                                                                       Transferase;
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--NSKFLLMVRDGRASVHSMITR

271

--GKWVEADPHLRLIREVCRSHVRIAEAATLKPPPFLRGRYRL

-MEVGKEKCLP

--IEVMYAQC-

GFDLSSYRDCLTKWNKA-

KVTIA-

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GPILARDNGIVLGTN--

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-AVRDL

FYLMEPAWHVWTTLSQGSAATLHM-

--SKSGREKLRLDEAGVTD

| | | : : : | | AMQAFILEVIAKHGEPARVLCN

IFLCDMDVFDAYMPQSRNLSAFFNWATSRALCSPPACSAFPRGTISKQ-DVCKTLCT

RSGTTLMRAMLDAHPEVRCGEETRIIPRVLAMRQAW-

RSGSSFLGQLFSQHPDV

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WRHALPFTKILRVQEVCAGALQLLGYRP

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VRFEDLAREPLAEIRALYAFTGLTLTPQLEAWIHNITHGSG-IGKPIEAFHTSSRNARNV

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                                                                                                                                                                                                                      ning and expression of human and mouse tyrosylprotein se-2 and a tyrosylprotein sulfotransferase homologue selegans."; 273:24770-24774(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTE).
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LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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TISSUE SPECIFICITY: WIDELY EXPRESSED.
SIMILARITY: BELONGS TO THE PROTEIN SULFOTRANSFERASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
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of distinct tyrosylprotein sulfotransferase genes: characterization of tyrosylprotein sulfotransferase. Acad. Sci. U.S.A. 95:11134-11139(1998).
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Blum H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE=Brain;

MEDLINE=21154917; PubMed=11230166;

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CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate +
adenosine 3',5'-bisphosphate + protein tyrosine-
SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> L (IN REF. 5)
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V -> E (I
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PF00685; Sulfotransfer; 1.
erase; Transmembrane; Glycoprote
                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=98406128; PubMed=9733778;
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; AF049891; AAC36061.1; -
; AJ006198; CAA06906.1; -
; Z95115; CAB62950.1; -
; AL136623; CAB66558.1; -
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                                                                                                                                                                                            Ouyang Y.-B., Moore K.L.; "Molecular cloning and ex| sulfotransferase-2 and a Caenorhabditis elegans.";
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Submitted (MAY-1998)
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(DEC-1999)
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                                                                    . Natl. Acad.
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CARBOHYD
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SEQUENCE
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                                                                                                                                                                   Mononegaviral
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                                                                                                                                                                                                                                                           disease virus.";
91:4362-4366(1994).
PROBABLY A COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase.
                                                                                                                                                                                                                                                                                                        triphosphate
                                                             RRPL_BDV
P52639;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
RNA polymerase beta subunit (EC 2.7.7.48) (Large rentein) (P180).
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 86.5;
Pred. No. 1
                                                                                                                                                                    viruses;
                                                                                                                                                                                                                                      A.J.,
                                                                                                                                                                                                                                                                                                          nucleoside
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                                                                                                                                                                                                                           PubMed=8183914;
ann A., Lewis A
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U04608; AAA20228.1; -.
InterPro; IPR001016; Paramyx_RNPPfam; PF00946; Paramyx_RNA_pol;
Transferase; RNA-directed RNA posecure 1608 AA; 180254 MW;
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rad. Sci. U.S.A. 9
THIS PROTEIN IS F
                                                                                                                                                       disease virus (BDV).
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ilarity 23.7%;
Conservative 3
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Briese T., Schneemann A.,
Ludwig H., Lipkin W.I.;
"Genomic organization of E
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                                                                                                                                                                                                                                                                                               POLYMERASE.
CATALYTIC ACTIVITY:
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                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                               NCBI_TaxID=12455;
                                                                                                                                                                                                                                                                           Acad
                                                                                                                                                                                                                                                                                    FUNCTION:
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Best Local S
Matches 64
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                                                                                                                                                                      Viruses;
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14

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Gap

123;

Indels

110;

Mismatches

36;

Conservative

73;

Matches

Similarity

Match

Query Match Best Local

377;

Length

DB 1;

Score 86.5; 1 Pred. No. 2.5

4.2%; 21.3%;

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    -HLRLIREVCRSHV
                            -DAGPGVIRLDRLESVCYAHP
                                                                 |: :| || |: |||
-LEFNAYLDS--ELVDISDMCCLPLATPCKALFRPIYRSLQSFRLALMDNYSFV
                                                                                                      -GKPIEAFHTSSRNAR
                                                                                                                        MDLIMIRGLDIRPHLEEFDELLVVGQHILGQPVLVEVVYYVGVVRKRPVLARHPWSADLK
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=ATCC 17965 / Melassecola;

MEDLINE=96345604; PubMed=8755867;

Ankri S., Serebrijski I., Reyes O., Leblon G.;

"Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: a natural bypass of the proA step.";

J. Bacteriol. 178:4412-4419(1996).

-! SIMILARITY: SOME, TO B.SUBTILIS OBG C-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL
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EKAESVIIKPKAVVHRTKGQFQIKPDPEVQGGFIITGEKPERWILQTDFENDEAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBIthe European Bioinformatics Institute. There are no restric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no resignating as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in proB 5'region (Fragment).
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                      -IRALYAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A0CA77DB6DF3DB02 CRC64
    DNGIVLGTNGKWVEADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88;
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                        YERLLEMDLCGAVSSRVDIPHSLAGRIHRGFAVGP---
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                                                RIAEAATLKPPPFLRGRYRLVRFEDLAREPLAE-
                                                                                                                                                     358
                                                                                                                                                                                                                                                                              Last sequence up
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000765; GTP1_OBG.
905; GTP1_OBG; PARTIAL.
                                                                                                                                                                                                                                         PRT;
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V--LRSREAAGPILAR
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PROSITE; PS00905; GT
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...-OCT-2001 (Rel. 4
Hypothetical pro
Corynebactor
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53; Conser
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Corynebacterium.
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TaxID=1718;
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P46584;
01-NOV-1995
01~NOV-1995
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collaboration -
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http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                   with the human cDNA.";

Nucleic Acids Res. 18:4925-4925(1990).

-!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE CONVERSION OF PYRUVATE COMPONENTS: PYRUVATE DEHYDROGENASE (E1), DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on
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-CLTLYGDGAANQGQIFEAYNMAALWKLPCVFICENNRYGMGTSVERAAASTD
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                                                                                                                                                           omatic form,
) (Fragment)
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Sus.
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PYRUVATE DEHYDROGENASE E1 COMPONENT
ALPHA SUBUNIT, SOMATIC FORM.
PHOSPHORYLATION (BY SIMILARITY).
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PHOSPHORYLATION (BY SIMILARITY)
PHOSPHORYLATION (BY SIMILARITY)
E9C7DF85389A9A47 CRC64;
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EAFHTSSRNARNVSQAWRHALPFTKILRVQEVCAGALQLLGYRPVYSADQQR
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ne PDH-El alpha
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                                                                                                                                                          lpha subunit,
(PDHE1-A type
                                                                                                                                                                                                         Chordata; Craniata; Vertebrata
Cetartiodactyla; Suina; Suidae
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                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Pyruvate + lipoamide = Sacetyldihydrolipoamide + CO(2).
COFACTOR: THIAMINE PYROPHOSPHATE.
ENZYME REGULATION: E1 ACTIVITY IS REGULATED (INACTIVATION) AND DEPHOSPHORYLATION (ACTIVE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT.
SUBCELLULAR LOCATION: Mitochondrial matrix.
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Flavoprotein;
''on; Transit pe
                                                                                            389
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Muscle;
MEDLINE=90370488; PubMed=2395657;
Sermon K., Demeirleir L., Elpers I., Lis
                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Pyruvate dehydrogenase El component al
mitochondrial precursor (EC 1.2.4.1)
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Pred.
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ilarity 17.5%;
Conservative 4
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S20813; DEPGPA.
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                            RISAAERK
                                                                                          STANDARD;
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389
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292
299
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Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
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Phosphorylation;
NON_TER 1
TRANSIT <1
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                          RLEQTS
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GKDEV
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P29804;
01-APR-19
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InterPro;
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Best Local S
Matches 47
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SEQUENCE
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MOD_RES
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7;

qq	241 YYKRGDFIPGLRVDGMDI	258
QY	FSLAREACRSYS	/L 209
qq	259LCVREATRFAAAYCRSGKGPILMELQTYRYHGHSMSDPGVSY 300	3X 300
ΩY	AGPIL	261
QQ	IED	9F 360
QΥ	262PPF-LRGRYRLVRFEDLA 278	
Dp	361 EELGYHIYCNDPPFEVRGANQWIKFKSIS 389	

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sw model using protein search, 1 OM protein

time 21.22 Seconds alignments)
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390

... LTLDLVLPRGPDHFSWASPD

Title: Perfect s Sequence:

MWLPRESSKTVTVLLLAQTT. US-09-593-828-8 2051 1 MWLPRFSSKTVTVT. score:

BLOSUM62 Gapop 10.0 , Scoring table:

residues 0.5 96089334 Gapext ` 283138 seqs, Searched:

283138 hits satisfying chosen parameters of Total number

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Database

PIR_71:*
1: pir1:*
2: pir2:*
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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. j.S Pred. score and is

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JE0261
N-acetylglucosamine-6-0-sulfotransferase
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05
C;Accession: JE0261
R;Uchimura, K.; Muramatsu, H.; Kaname, T.
T.
                                                                                                A; Reference number: JE0261; MUID: 9839184:
A; Accession: JE0261
A; Molecule type: mRNA
A; Residues: 1-484 <UCH>
A; Cross-references: DDBJ: AB014679
C; Comment: This protein catalyzes the trace; C; Keywords: sulfotransferase
                                                                                                                                                                                                                                                                                                                                                         -REAAGPILARD-
                                                                   J. Biochem. 124, 670-678, 1998
A; Title: Human N-Acetylglucosamine-6
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ilarity 40.0%;
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A57397
chondroitin 6-sulfotransferase (EC 2.8.2.17) pre
C; Species: Gallus gallus (chicken)
C; Date: 23-Feb-1996 #sequence_revision 23-Feb-19
C; Accession: A57397
R; Fukuta, M.; Uchimura, K.; Nakashima, K.; Kato,
J. Biol. Chem. 270, 18575-18580, 1995
A; Title: Molecular cloning and expression of chi
A; Reference number: A57397; MUID:95355490
A; Accession: A57397
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-458 <FUK>
C; Superfamily: chondroitin 6-sulfotransferase
C; Keywords: sulfotransferase
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C;Comment: This enzyme, having a type II transmembrane topology and N-linked
sulfate linkage formation. This enzyme is involved in synthesis of L-select:
C;Keywords: glycolysis; sulfate transport; sulfotransferase; transmembrane p
                                                                 N-acetylglucosamine-6-O-sulfotransferase (EC 2.8.2.-) [validated] - mouse (5.5pecies: Mus musculus (house mouse) (5.5pecies: Massukawa, T.; Kacession: JC7350 (5.4cession: JC7350 (5.5pecies: Matsukawa, T.; Yamakawa, T.; Ku Biochem. Biophys. Res. Commun. 274, 291-296, 2000 (7.5pecies: Molecular of A; Reference number: JC7350; MuID:20374462 (7.5pecies: Molecule type: mRNA (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75) (7.75)
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Pred. No. 2.8e-47;
54; Mismatches 127;
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G70729
hypothetical protein Rv2267c - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 22-Oct-1999
C; Accession: G70729
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Conoc, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holl Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                         PIDN: AAA91354.1;
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                                                              hypothetical protein F42G9.8 - Caenorhabditis elega
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999
C;Accession: T16350
                                                                                                                                                                                                                                                                                                                                                                                 220/3; 290/2
hypothetical
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Pred. No. 0.14;
3; Mismatches 1
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source: strain Bristol N2
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|--RLYP
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The sequence of C. elegans
ber: Z18498
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Similarity 19.8%;
80; Conservative
                                                                            C; Species: Caenorhabditis elegan
C; Species: Caenorhabditis elegan
C; Date: 20-Sep-1999 #sequence_re
C; Accession: T16350
R; Taich, A.
submitted to the EMBL Data Libra
A; Description: The sequence of C
A; Reference number: Z18498
A; Accession: T16350
A; Status: preliminary; translate
A; Molecule type: DNA
A; Experimental source: strain Bi
C; Genetics:
A; Genetics:
A; Genetics:
A; Introns: 28/2; 50/2; 113/2; 15
C; Superfamily: Caenorhabditis el
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∵.:
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C;Species: Sinorhizobium mellioti
R;Finan, Tan.; Weinder, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J
R;Finan, Tan.; Weinder, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J
R;Finan, Tan.; MulD:21396508; PMID:11481431
A;Status: preliminary
A;Scession: E95934
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78; Conservative
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probable valine--pyruvate transaminase (E
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03
C; Accession: T38905
R; Connor, R.; Churcher, C.M.; Barrell, B.
submitted to the EMBL Data Library, Septe
A; Reference number: Z21813
A; Accession: T38905
A; Reference number: Z21813
A; Accession: T38905
A; Experiment at type: DNA
A; Residues: 1-474 <CON>
A; Residues: 1-474 <CON>
A; Experimental source: strain 972h-; cosm
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F; 1-27/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F; 28-388/Product: pyruvate dehydrogenase (lipoamide) alpha chain #status F; 183-232/Domain: thiamin pyrophosphate-binding domain homology <TPB>
F; 230/Binding site: phosphate (Ser) (covalent) #status predicted F; 298/Binding site: phosphate (Ser) (covalent) #status predicted F; 298/Binding site: phosphate (Ser) (covalent) #status predicted
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A testis-specific form of the human pyruvate
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larity 23.2%; Pred. No.
Conservative 25; Mismato
A; Cross-references: GB:Z77163; GB:AL123456; A; Experimental source: strain H37Rv
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A; Molecule type: mRNA
A; Residues: 1-388 <DAH>
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A;Cross-references:
C;Genetics:
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Cross-references: EMBL:M29232; NID:g168271; PIDN:AAA33
Superfamily: histidine ammonia-lyase
Keywords: ammonia-lyase; carbon-nitrogen lyase
192-194/Cross-link: 5-imidazolinone (Ala-Gly) #status
193/Modified site: dehydroalanine (Ser) #status predic
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Pred. No. 2.2;
6; Mismatches
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September
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e: strain 972h-; cosmid c
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                                                                                                                                                                                                                                                                    RESULT 9
$29029
phenylalanine ammonia-lyase (EC 4.3.1.5) - s
C; Species: Ipomoea batatas (sweet potato)
C; Date: 25-Feb-1994 #sequence_revision 10-Nc
C; Accession: $29029
R; Tanaka, Y.; Matsuoka, M.; Yamanoto, N.; OP
Plant Physiol. 90, 1403-1407, 1989
A; Title: Structure and characterization of a
A; Reference number: $29029
A; Reference number: $29029
A; Molecule type: mRNA
A; Residues: 1-707 <TAN>
C; Superfamily: histidine ammonia-lyase
C; Superfamily: histidine ammonia-lyase
C; Keywords: ammonia-lyase; carbon-nitrogen 1
F; 192-194/Cross-link: 5-imidazolinone (Ala-G F; 193/Modified site: dehydroalanine (Ser) #s
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Length

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DB

OY 102 LCDMDVFDAXMPQSRNLSAFFNWATSRALCSPPACSAFPRGTISKQDVCKTLCTRQPFSL 161 1	REGULT 12 VARDAY Upplomer glycoprotein precursor - herne virus (strain p.38/72) C. Date: 30-30m.1991 #sequence_revision 30-3un-1991 #text_change is-Jul-1999 C. Accession: ASG792 ben Boon, A.; Spear, W.J.M.; Weiss, M.; Horzinek, M.C. A. Title: Primary structure and post-translational processing of the Berne virus pepto A. Accession: ASG792; MJD: 9102093 A. Accession: ASG792; MJD: 9102093 A. Accession: ASG793; MJD: 9102093 A. Accession: ASG794; MJD: 9102093 A. Accession: ASG795; MJD: 910209 A. Accession: ASG795; MJD: 910209 A. Accession: ASG795; MJD: Accession: Accession
Best Local Similarity 22.3%; Pred. No. 1.6; Matches 69; Conservative 48; Mismatches 125; Indels 68; Gaps 17; OY 33 SSPAGGEDRVHVLVLSS	RESGLE 11 S72346 S72347

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                                                                                                                                          source
                                                           preliminary
                                                                                   DNA
                       Reference number:
Accession: C75278
                                                                               Molecule type: I
Residues: 1-615
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A; Title: Genome
A; Reference numb
A; Accession: C75
A; Status: prelim
A; Molecule type:
A; Residues: 1-61
A; Cross-referenc
A; Experimental s
C; Genetics:
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N.; Holroyd
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Zalewski,
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complete
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probable oxalyl-CoA decarboxylase - Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-201-1998 #sequence_revision 17-301-1998 #text_change 20-Jun-2000
C;Accession: A70841
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; C, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hol; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70801
A;Reference number: A70801
A;Reference number: A70801
A;Reterence number: B70801
A;Residues: DNA
A;Residues: 1-582 <COL>A;Residues: 1-5
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                                                                    HP--AGVIMIARHHSMWSVAARNSTSFYCVTHSLITFGKLDISTSWFFHTLALPSGPVSQ
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R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
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                                                                                                                                                                                                               ; Score 94; DB 2; Pred. No. 2.6; 44; Mismatches
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                                                                                                               GLTLTPQLEAWIHNIT
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Best Local Similarity 21.4%;
Matches 55; Conservative
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-EGRLEGAEVPRLL
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                                                                      PIDN: AAF11
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K.R.; Kas,
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Title: Complete genome sequence of Pseudomonas
Reference number: A82950; MUID:20437337
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the radioresistant MUID:20036896
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PAO1
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No. 3.
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Coulter,
                                                                                                                                       polymerase
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C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15
C; Accession: B83629
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter
.; Lory, S.; Olson, M.V.
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il Similarity 23.4%;
92; Conservative 41
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                                                           Residues: 1-615 <WHI>
Cross-references: GB:AE002071;
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                                                                                                                                       DNA
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                                                                                                              Gene: DR2410
Map position: 1
Superfamily: DNA-directed
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Search completed: September 20, 2002, 19:58:58 Job time: 147 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 20, 2002, 19:56:06; Search time 14.8 Secon

, 19:56:06; Search time 14.8 Seconds (without alignments) 643.647 Million cell updates/s

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390

Title: US-09-593-828-8
Perfect score: 2051
Sequence: 1 MWLPRFSSKTVTVLLLAQTT...

Sequence: 1 MWLPRFSSKTVTVLLLAQTT.....LTLDLVLPRGPDHFSWASPD Scoring table: BLOSUM62

g table: BLOSUM62
Gapop 10.0 , Gapext

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Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

essing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued_Patents_A

: Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TIMMARTES

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		Match	Length	DB		escript
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15	0		∞	4	-09-374-492-	quence 3, Appl mence 9 Anni
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equence 41, App equence 41, App	цς	equence 41, App	equence 10, App	e 10, App	equence 10, App	guence 36. App	equence 2. Anni	guence 69. Ann	edilence 54 App	edilence 66. Ann	ednence 75. App	equence 89. Ann	Adri // Compension of the desired of	guence 23, APP	equence 23, App
4-158B-4-596A-	-08-458-731-41	-149-223A-4	S - 08 - 3	-08-582-776C-1	-08-434-831B-	-09-108-020-3		-08-444-818-6	18 - 5	8 - 6	18-7	18-8	6 - 975A - 2	~08-391-671A-2	-08-467-902A-
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ALIGNMENT

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RESULT 1
US-09-045-284A-2
Sequence 2, Application US/09045284A
Patent No. 6265192
GENERAL INFORMATION:
APPLICANT: Bistrup, Annette
APPLICANT: Rosen, Steven D.
APPLICANT: Hemmerich, Stefan
TITLE OF INVENTION: GLYCOSYL SULFOTRANSFERASE-3
FILE REFERENCE: 6510-107US1
CURRENT APPLICATION NUMBER: US/09/045,284A
CURRENT FILING DATE: 1998-03-20
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 386
TYPE: PRT
CORGANISM: Homo sapiens
US-09-045-284A-2
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118 120 178 180 240 Gaps 59 9 SAFFNWATSRALCSPPACSAFPRGTISKODVCKTLCTRQPFSLAREACRSYSHVVLKEVR 28; 386; Indels Length Score 1008; DB 4; Pred. No. 1.1e-102; ; Mismatches 104; 56; 49.1%; ilarity 52.3%; Conservative 5 LLLAQTTCLLLFIISRP-1 Similarity 206; Conser Query Match Best Local S Matches 206 14 9 61 \vdash 119 121 179 181 g QQ QYqq ă Ω Q_{Y} a

LGYRPVYSADQQRDLTLDLVLPRGPDHFSWASPD 390

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Mismatches
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ADDRESSEE: KNOBBE, MARTENS, OLSON
STREET: 620 NEWPORT CENTER DRIVE,
CITY: NEWPORT BEACH
STATE: CALIFORNIA
                                                                                                                                                                        ^{\circ}
                                                                                                             10-54007
                                                                                                                                                                        Version
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Pred.
APPLICANT: Kadomatsu, Kenji
APPLICANT: Kannagi, Reiji
APPLICANT: Habuchi, Osami
APPLICANT: Huramatsu, Takashi
TITLE OF INVENTION: POLYPEPTIDE OF
TITLE OF INVENTION: DNA ENCODING TH
FILE REFERENCE: TOYAM41.001AUS
CURRENT APPLICATION NUMBER: US/09/2
CURRENT FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: JP 10-5
EARLIER APPLICATION NUMBER: JP 10-1
EARLIER APPLICATION NUMBER: JP 10-1
EARLIER FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 10
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GENERAL INFORMATION:
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CITY: NEWPO
STATE: CALI
COUNTRY: US
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CCANT: Habuchi, Osami

CCANT: Habuchi, Osami

CCANT: Muramatsu, Takashi

E OF INVENTION: POLYPEPTIDE OF N-ACETYLGLUCOSAMINE-6-0-SULFOTRANSF

E OF INVENTION: DNA ENCODING THE SAME

REFERENCE: TOYAM41.001AUS

ENT APPLICATION NUMBER: US/09/263,023

ENT FILING DATE: 1999-03-05
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-64;
121;
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Pred. No. 1.1e-6
4; Mismatches 1
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CURRENT FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: JP 10-54007
EARLIER FILING DATE: 1998-05
EARLIER APPLICATION NUMBER: JP 10-177844
EARLIER FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --REAAGPILARD----
                                                                  -09-263-023-2
Sequence 2, Application US/09263023
Patent No. 6037159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/0926302
Patent No. 6037159
GENERAL INFORMATION:
APPLICANT: Uchimura, Kenji
APPLICANT: Muramatsu, Hideki
                                                                                                                                                                                                                                                                                                                                                                                                                          64;
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40.4%;
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Muramatsu, Hideki
Kadomatsu, Kenji
          Conservative
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Matches 150; Conser
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TITLE OF IN
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APPLICANT: FUKUTA, MASAKAZU
TITLE OF INVENTION: POLYPEPTIDE OF GLYCOSAMINOGLYCAN
TITLE OF INVENTION: SULFOTRANSFERASE ORIGINATING FROM HUMAN AND DNA
TITLE OF INVENTION: FOR THE POLYPEPTIDE
NUMBER OF SEQUENCES: 9
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SULFOTRANSFERASES, NUCLEIC ACIDS
SULFOTRANSFERAES, AND METHODS OF
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-IRLSAELGL
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                                                                                                                    5,87
                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6060295
GENERAL INFORMATION:
APPLICANT: The Board of Regents of tl
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                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TITLE OF INVENTION: TYROSYLPROTEIN
TITLE OF INVENTION: TYROSYLPROTEIN
                                                                                                                                                                                       NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                INFORMATION
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TRNGTH: 458
                                                  COMPUTER READABLE FORM:
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MOLECULE TYPE: 08-655-878-2
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COUNTRY:
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                                                                                                                                                                                                                                                                                                  Score 577.5; DB 2;
Pred. No. 4.7e-55;
5; Mismatches 134;
                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 714 760 9502
FORMATION FOR SPORT
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IBM PC compatible
YSTEM: PC-DOS/MS-DOS
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HABUCHI, OSAMI
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35.7%;
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                                                   CURRENT APPLICATION DATA APPLICATION NUMBER: U
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  FORM:
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                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA
APPLICATION NUMBER:
                                           PatentIn
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                             OPERATING SYSTEM:
SOFTWARE: Patent
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APPLICANT: FUKUTA
APPLICANT: HABUCH
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RSVSLLEERG
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MOLECULE TYPE: -08-899-514-2
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                     COMPUTER:
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SULFOTRANSFERASES, NUCLEIC ACIDS
SULFOTRANSFERAES, AND METHODS OF
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-NAKFILMIRDARAVVHSMI
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1998-09-09
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FILE REFERENCE: 5820.504
CURRENT APPLICATION NUMBER: UCURRENT FILING DATE: 1998-09-NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 5.1 (SE
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CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 1998-09
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 5.1 (s
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CURRENT APPLICATION NUMBER: US/09/374,493
CURRENT FILING DATE: 1999-08-13
EARLIER APPLICATION NUMBER: 09/150,133
EARLIER APPLICATION NUMBER: 60/072,994
EARLIER FILING DATE: 1998-01-29
EARLIER APPLICATION NUMBER: PCT/US99/16750
EARLIER FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 8.0 (saved in ASCII for
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APPLICANT: The Board of Regents of the University of INVENTION: TYROSYLPROETIN SULFOTRANTILE OF INVENTION: TYROSYLPROETIN SULFOTRANTILE REFERENCE: 5820.547

CURRENT FILING DATE: 1999-08-13

EARLIER APPLICATION NUMBER: 60/072,994

EARLIER APPLICATION NUMBER: 60/072,994

EARLIER FILING DATE: 1998-01-29

EARLIER FILING DATE: 1998-01-29

EARLIER FILING DATE: 1999-07-23
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Patent No. 6207432
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R APPLICATION NUMBER: 60/07
R FILING DATE: 1998-01-29
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APPLICANT: The Board of Regents of the University Title OF INVENTION: TYROSYLPROETIN SULFOTRANG FILE REFERENCE: 5820.545
CURRENT APPLICATION NUMBER: US/09/374,492
CURRENT FILING DATE: 1999-08-13
EARLIER APPLICATION NUMBER: 09/150,141
EARLIER FILING DATE: 1998-09-09
EARLIER FILING DATE: 1998-01-29
EARLIER FILING DATE: 1998-01-29
EARLIER FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 45
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Fatent No. 6060295
GENERAL INFORMATION:
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANS
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANS
FILE REFERENCE: 5820.504
CURRENT APPLICATION NUMBER: US/09/150,133B
CURRENT FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 5.1 (saved in ASCII for
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GENERAL INFORMATION:

TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANS

TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANS

FILE REFERENCE: 5820.495

CURRENT APPLICATION NUMBER: US/09/150,141B

CURRENT FILING DATE: 1998-09-09

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Wordperfect 5.1 (saved in ASCII for
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GENERAL INFORMATION:

TITLE OF INVENTION: TYROSYLPROETIN SULFOTRAN;

FILE REFERENCE: 5820.547

CURRENT APPLICATION NUMBER: US/09/374,824

CURRENT FILING DATE: 1999-08-13

EARLIER APPLICATION NUMBER: 60/072,994

EARLIER APPLICATION NUMBER: 60/072,994

TILING DATE: 1998-01-29
                                                                                                                  APPLICANT: The Board of Regents of the Univer TITLE OF INVENTION: TYROSYLPROETIN SULFOTRANS FILE REFERENCE: 5820.546
CURRENT APPLICATION NUMBER: US/09/374,493
CURRENT FILING DATE: 1999-08-13
EARLIER APPLICATION NUMBER: 09/150,133
EARLIER FILING DATE: 1998-09-09
EARLIER FILING DATE: 1998-01-29
EARLIER FILING DATE: 1998-01-29
EARLIER FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 8.0 (saved in ASCII for
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No. 6204016
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; Patent No. 6207432

; GENERAL INFORMATION:

; APPLICANT: The Board of Regents of the University of INVENTION: TYROSYLPROETIN SULFOTRAN

; TITLE OF INVENTION: TYROSYLPROETIN SULFOTRAN

; FILE REFERENCE: 5820.545

; CURRENT APPLICATION NUMBER: US/09/374,492

; EARLIER APPLICATION NUMBER: 09/150,141

; EARLIER FILING DATE: 1998-09-09

; EARLIER FILING DATE: 1998-01-29

; EARLIER FILING DATE: 1999-07-23

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: Wordperfect 8.0 (saved in ASCII f
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EARLIER APPLICATION NUMBER: PCT/US99/16750
EARLIER FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 45
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(GST-4alpha) sulfotransferase-4alpha glycosylHuman

Human; glycosyl sulfotransferase-4alpha; GST-4alpha; immunosuppressive; therapy; selectin binding inhibitor; gene therapy; inflammation; systemic lupus erythematosus; SLE; rheumatoid arthritis; diabetes; polyarteritis nodosa; polymyositis; systemic sclerosis; dermatitis; glomerulonephritis; myasthenia gravis; Sjogren's syndrome; adrenalitis; Hashimoto's disease; Grave's disease; hypoparathyroidism; anaemia; demyelinating disease; cirrhosis; ulcerative colitis; allergic rhinitis; myocarditis; adult respiratory distress syndrome; eczema; psoriasis; asthma; hypersensitivity; rheumatic fever; tissue rejection; chromosome 16q23.1.

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99US-0144694. 2000US-0593828.)-JUL-1999; 3-JUL-2000; 0

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The present sequence is human glycosyl sulfotransferase-4alpha (GST-4 alpha). GST-4 gene is found on chromosome 16q23.1.

GST is a type 2 membrane protein useful for inhibiting a binding event selectin and a selectin ligand, which comprises contacting the selectin with a non-sulphated selectin ligand, which comprises contacting the agent that inhibits the sulphation activity of GST as as and molecular agent that inhibits the sulphation activity of GST is useful in gene therapy to treat disorders such as acute or chronic inflammation, systemic lupus erythematosus (SLE), rheumatoid arthritis, polyarteritis nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes, glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's disease, Grave's disease, adrenalitis, hypoparathyroidism, pernicious anaemia, demyelinating diseases, cirrhosis, ulcerative colitis, canaemia, amyocarditis, regional enteritis, adult respiratory distress syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis, bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection of where mhe ancest.
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Leach M; RA, Shimkets

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× derived from open reading, proliferative disorders, sardiovascular disease , proliferative cardiovascular d cancers, and peptides and nucleic acids and pept for treating e.g. car legenerative disorders neurodegenerative Novel nsetı

English. 5507pp; 2599-2600; Page 11;

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatclogical; immunosuppressive; antidiabetic; hypotensive; dermatclogical; immunosuppressive; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating the precipitative disorders, neurodegenerative disorders, neurodegenerative disorders, osteoarthritis, proliferative disorders, neurodegenerative disorders, osteoarthritis, cardinates and nucleic acids may be used to treat cancers, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coamulation; to inhibit thrombosis; and se a contranentive. $_{
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The present sequence is human glycosyl sulfotransferase-4beta (GST-4 beta). GST-4 gene is found on chromosome 16q23.1.

GST is a type 2 membrane protein useful for inhibiting a binding event between a selectin and a selectin ligand, which comprises contacting the selectin with a non-sulphation activity of GST and a small molecular agent that inhibits the sulphation activity of GST. GST is also useful in inhibiting a selectin mediated binding event. GST is useful in gene therapy to treat disorders such as acute or chronic inflammation, condosa, polymyositis, dermatomyositis, rheumatoid arthritis, polyarteritis glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's anaemia, demyelinating disease, cirrhosis, ulcerative colitis, dermatitis, myocarditis, regional enteritis, adult respiratory distress bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection
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                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                 1729.5; DB 22
No. 5.1e-181;
ematches 37;
                                                                                                                                                                                                                                                                                       Score 1729.5;
Pred. No. 5.1e
7; Mismatches
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ilarity 85.8%;
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Best Local Similarity
Matches 333; Conser
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bronchial asthma,
during transplanta
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for

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GST

and

uses (GST)-4alpha, GST-4beta agent screening applications

rl sulfotransferases and theranometric

glycosyl

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AAD02700

01-138471/14. AAD02697, AA

WPI; 2001-N-PSDB; AA

English

128pp;

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The present sequence is mouse glycosyl sulfotransferase-4 (GST-4). GST-4

gene is found on chromosome BEI.

GST is a type 2 membrane protein useful for inhibiting a binding event

between a selectin and a selectin ligand, which comprises contacting the

selectin with a non-sulphated selectin ligand, GST and a small molecular

agent that inhibiting a selectin mediated binding event. GST is useful

in inhibiting a selectin mediated binding event. GST is useful

therapy to treat disorders such as acute or chronic inflammation,

therapy to treat disorders such as acute or chronic inflammation,

systemic lupus erythematosus (SLE), rheumatoid arthritis, polyarteritis

nodosa, polymyositis, dermatomyositis, systemic sclerosis, diabetes,

glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's

disease, Grave's disease, adrenalitis, hypoparathyroidism, pernicious

anaemia, demyelinating diseases, cirrhosis, ulcerative colitis,

dermatitis, myocarditis, regional enteritis, adult respiratory distress

syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis,

bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection

conting transplantation.
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                                                                                                                                                                                                                                                                                                                          ases (GST)-4alpha, GST-4beta agent screening applications
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Pred. No. 8.2e-160;
; Mismatches 62;
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1 Similarity 76.0%;
295; Conservative
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2000US-0593828
                                                                                                                              2000WO-US19741
                                                                                                                                                                                                                                                                                                                                              therapeutic
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)B; AAD02696.
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chromosome 8E1
                                                               WO200106015-A1
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3-JUL-2000;
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                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                           The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length clones were obtained by construction of full length clones were obtained by construction of flength enriched cDNA libraries that were synthesised by the oligo-c method. The primers enable the production of the full length cDNA encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the precification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAFFNWATSRALCSPPACSAFPRGTISKODVCKTLCTROPFSLAREACRSYSHVVLKEVR
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T, Koga
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S, Otsuki
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..6e-102;
les 104;
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K, Kojima
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Mismatches
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Pred. No. 2
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T, Nagai
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ilarity 52.5%;
Conservative 5
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2000JP-0118774
2000JP-0183765
                                                              Protein;
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les 207; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the invention. The nucleic acid sequences, probes and primers derived from these, proteins and antibodies are useful in detecting homologues. The sequences, antibodies are useful in the diagnosis and treatment of diseases associated with selectin binding interactions, including conditions associated with or resulting from the homing of leukocytes to sites of inflammation and the normal homing of lymphocytes to secondary lymph organs.
                                                                                                                                                                                                                                                                                            leukocyte homino
oming; human;
      180
                        237
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                  FFNLQVLYPLLSDPALNLRIVHLVRDPRAVLRSREAAGPILARDNGIVLGTN-GKWVEAD
{\tt sslfqwensralcsapacdiipqdeiiprahcrllcsqqpfevvekacrsyshvvlkevr}
                                                         PHLRLIREVCRSHVRIAEAATLKP-PPFLRGRYRLVRFEDLAREPLAEIRALYAFTGLTL
                                                                   TPQLEAWIHNITHGSGIGKPIEAFHTSSRNARNVSQAWRHALPFTKILRVQEVCAGALQL
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binding interaction;
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qpyyvmqvicqsqleiyk--tiqslpkalqeryllvryedlarapvaqtsrmyefvglef
                                                                                                                                                                                                                                                                                                                       Transferase; TRNSFS-11; human; antitumour; cell proliferation; gastrointestinal disorder; developmental disorder; genetic disorder; neurological disorder; reproductive disorder smooth muscle disorder; immunological disorder; inflammation; diagnosis; therapy; N-acetylglucosamine 6-0-sulfotransferase.
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Score 1008; DB 20; Pred. No. 9.4e-102; 5; Mismatches 104;

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49.1%; larity 52.3%; Conservative

Query Match Best Local Similarity Matches 206; Conser

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                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of human transferase TRNSFS-11, 1 of 15 claimed novel human transferase proteins of the invention (see AAY79209-23). The sequence was deduced from a cDNA clone (see AAZ94211) isolated from a gallbladder library. It shows homology to mouse N-acetylglucosamine 6-0-sulfotransferase. TRNSFS-11 is expressed in dermatologic and gastrointestinal tissues, especially those associated with inflammation and cell proliferation. The new human transferases and polynucleotides can be used in the diagnosis, prevention and treatment of cancer, developmental disorders, gastrointestinal disorders, genetic disorders, immunological disorders, neurological disorders, reproductive disorders, and smooth muscle disorders. The polypeptides can also be used to raise antibodies, and to screen of transferase activity.
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1.4e-97;
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and developmental,
                               "potential
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Azimzai Y;
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N-PSDB; AAZ94211.
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04-NOV-1998;
11-MAY-1999;
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lymphocyte homing; mou
25;
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Pred. No. 2.6e
2; Mismatches
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on; inflammation;
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                                                                                                                                         sulfotransferase-3
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                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                        sulfotransferase; GS'
binding interaction;
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l Similarity 55.6%;
193; Conservative
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98US-0190911
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                                                                                        Protein;
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gyrhvrseqeqrnllldll
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B; AAZ20793.
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                                                                                                                                                                                                                                                                                                  USA
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polynucleotides
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                                                                                                                                           glycosyl
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12-NOV-1998;
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                                                                                                                                                          Glycosyl
selectin
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N-PSDB;
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(SYNT
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Matches
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ion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents mouse N-acetylglucosamine-6-0-sulfotransferase, an enzyme capable of transferring a sulfate group from a sulfate group donor to a hydroxyl group at the 6 position of an N-acetylglucosamine residue located at the non-reducing end of an oligosaccharide of formula GlcNAcbetal-3Galbetal-4GlcNAc, where GlcNAc = N-acetylglucosamine residue, Gal = galactose residue, beta 1-3 = beta 1-3 glycosidic linkage, and beta 1-4 = beta 1-4 slycosidic linkage. The enzyme is useful for the synthesis of sugar chains such as GlyCAM-1, a ligand of L-selectin that is involved in homing of lymphocytes and rolling of leukocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       harbour
                                                                  VCRSHVRIAEA-ATLKPPFFLRGRY
               RLVRFEDLAREPLAEIRALYAFTGLTLTPQLEAWIHNITHGSGIGKPIEAFHTSSRNARN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of N-acetylglucosamine-6-0-sulfotransferase, sugar chains, e.g. GlyCAM-1
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or the large=:
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                                                                                                                                  375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             occurring at the early stage of inflammation. DNA ence enzyme (see AAX87820) is expected to be used for the laproduction of N-acetylglucosamine-6-0-sulfotransferase artificial synthesis of GlyCAM-1 using transformants where
                                                                                                       VSQAWRHALPFTKILRVQEVCAGALQLLGYRPVYSADQQRDLTLDLV
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                                                                                                                                                                                                                                                                                                     N-acetylglucosamine-6-0-sulfotransferase; mouse;
L-selectin ligand.
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                                                                                                                                                                                                  483
RDNGIVLGTNGKWVEADPHLRLIRE
                                                                                                                                                                                                 standard; Protein;
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98JP-0054007
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for synthesis of
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05-MAR-1998;
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221
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       CKTLCTRQPFSLAREACRSYSHVVLKEVRFFNLQVLYPLLSDPALNLRIVHLVRDPRAVL
                                                                    GGEDRVHVLVLSSWRSGSSFLGQLFSQHPDVFYLMEPAWHVWTTLSQGSAATLHMAVRDL
                                     --NGKWVEADPH-LRLIREV
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                                                                                                                                                      SA
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                                                                                                   Yamamoto
T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                              -AFFNWATSRALCSPPACSAFPRGTISKQD
                                                                                                                                                                                                                                                                                                    gene
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n, and for the o
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Otsuki
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A, Nagai
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cDNAs defined in the s
(a) an oligo-dT primer
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T, Wakamatsu
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                          REAAGPILARD
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                                                                                                                                                                                                                                                                                     SEQ
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Sugiyama
                                                                                                                                                                                                                                        standard;
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/or diagnosis o
L-length cDNAs
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7-AUG-1999;
1-JAN-2000;
2-MAY-2000;
9-JUN-2000;
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full-le
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Ishii
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11;

Gaps

36;

Indels

Length 483;

Score 665; DB 20; Pred. No. 6.4e-64; Mismatches 121;

64;

Conservative

150;

Matches

Similarity

Local

Best

Query Match

32.4%; 40.4%; 22-SEP-1999

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y and sotides,
                                                                                                                                                                                                                              combination of
                                                                                                                                                                                                                                                                                                                                                                                 encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cation
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                      the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                     Y to
                                                                                                                                                                                                                                                                in
                                                                                                                       complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combinatithe 5'-end sequence/3'-end sequence is selected from those defined the specification. The primer sets can be used in antisense therap in gene therapy. The primers are useful for synthesising polynucle particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins enco
                                                                                               sequence complementary sotide which comprises
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AA; 530 Sequence

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12;
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                                                                                     264
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                   Gaps
                                   81
                                SQGSAATLHMAVRDLMRSIFLCDMDVFDAYMPQ~--SRNLS--AFFNWATSRALCSPPAC
                                                                                                  SAFPRGTISKQD--VCKTLCTRQPFSLAREACRSYSHVVLKEVRFFNLQVLYPLLSDPAL
                                                                                                                                           -NGIVLGTNGKWV
                                                                                                                                                                            TGLTLTPQLEAWIHNITHGSG-IGKPIEAFHTSSRNARNVSQAWRHALPFTKILRVQEVC
                                                                                                                                                                                                              | |:||| : ||| | :| :|:| | - fvvsarnatgaanawrtaltfqqikqveefc
                                                                                                                                                                   -EADPH-LRLIREVCRSHVRIAEAATLKPPPFLRGRYRLVRFEDLAREPLAEIRALYAF
   530;
  Length
                   Indels
 DB 22;
                122;
Score 659.5; D
Pred. No. 3e-63
                                                                                                                                    -REAAGPILARD-
         ed. No. 3e-
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               68;
32.2%;
39.1%;
                 Conservative
                                                                                                                                   NLRIVHLVRDPRAVLRS
        Similarity
               151;
Query Match
Best Local
                                                145
                                                                 82
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                Matches
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484 AA;

Sequence

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N-acetylglucosamine-6-0-sulfotransferase
                                                                 N-acetylglucosamine-6-0-sulfotransferase;
L-selectin ligand.
              AA
              484
             Protein;
                                         entry)
                                        (first
             standard;
                                                                                     sapiens
                                       09-NOV-1999
                          AAY31657;
            AAY31657
                                                    Human
1
                                                                                     Homo
RESULT
      AAY31
                         X
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The present sequence represents human N-acetylglucosamine-6-0-sulfotransferase, an enzyme capable of transferring a sulfate group from a sulfate group donor to a hydroxyl group at the 6 position of an N-acetylglucosamine residue located at the non-reducing end of an oligosaccharide of formula GlcNAcbetal-3Galbetal-4GlcNAc, where GlcNAc = N-acetylglucosamine residue, Gal = galactose residue, beta 1-3 = beta 1-3 glycosidic linkage, and beta 1-4 = beta 1-4 glycosidic linkage. The enzyme is useful for the synthesis of sugar chains such as GlyCAM-1, a ligand of L-selectin that is involved in homing of lymphocytes and rolling of leukocytes occurring at the early stage of inflammation. DNA encoding the enzyme (see AAX87821) is expected to be used for the large-scale production of N-acetylglucosamine-6-0-sulfotransferase, or artificial synthesis of GlyCAM-1 using transformants which harbour
                                                                                                                                                                                                                                              useful
                                                                                                                                                                                                                                                                                                                        represents human N-acetylglucosamine-6-0-enzyme capable of transferring a sulfate group donor to a hydroxyl group at the 6 position of ne residue located at the non-reducing end of formula GlcNAcbetal-3Galbetal-4GlcNAc, where cosamine residue, Gal = galactose residue,
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98JP-0054007
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K;
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Uchimura
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AAX87821.
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for synthesis of
                                                                                                                                                                                                                                                                                         Page
                                                                                                                                                             Τ,
                                                             -JUN-1998;
                               04-MAR-1999
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N-PSDB; AA
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"potential N-glycosylation
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/label= Transmembrane_domain
62..64
/label= Glycosylation
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95..97
/label= Glycosylation
'note= "potential N-gl"
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N-PSDB; AAT45037.
                                                                                                                                                                                                                                                                                                                                      standard;
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                                                    \Omega
                                            W06480) is capable of catalysing the transfer of a sulphate group a 3'-phosphoadenosine 5' phosphosulphate to the hydroxyl group the C-6 position of the N-acetylgalactosamine residue of a ration of the N-acetylgalactosamine residue of ration of the cDNA allows the mass prodn. of C6ST in transformed cells. Recombinant C6ST polypeptides are useful for analysing activities of chondroitin sulphate and for modifying its
                                                                                                                                                                                                                                                                                                                                                                                    -RDLMRSIFLCDMDVFDAYM---PQSRNLSAFFNWATSRALCSPPACSAFPRGTISKQD
                                                                                                                                                                                                                                                                       VCKTLCTRQPFSLAREACRSYSHVVLKEVRFFNLQVLYPLLSDPALNLRIVHLVRDPRAV
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-sulpho:transferase - for
e in industrial processes
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                                                                                                                                                                 18;
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141;
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                                                                                                                                                                 Score 540.5;
Pred. No. 2.8e
6; Mismatches
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                                                         from 3'-phosphoadenosine 5' at the C-6 position of the chondroitin. Its amino aci
                           18-20; 30pp;
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                                                                                       (AAT45037)
                                                      (AAW06480)
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This sequence produces the protein KSGal6ST (Keratan sulphate
6-sulphotransferase), which has a molecular weight of about 46700. The
6-sulphotransferase (cost) and using the cDNA of
cDNA sequence of this protein was obtained by radiolabelling the cDNA of
c chick chondroitin 6-sulphotransferase (cost) and using this as a probe in
a random oligonucleotide-primed labelling method. Human foetal brain
c clones containing the KSGal6ST were obtained by hybridization using the
c prepared probe. The positive clones were subcloned into a recombinant
c expression vector and used to transform cos-7 cells, from which cells
expressing KSGal6ST can be selected. The phage cDNA inserts were
c isolated and subcloned into a Bluescript plasmid. Deletion clones were
then prepared from which both strands were sequenced by the Sanger
method. The KSGal6ST of the invention transfers the sulphate from a
sulphate donor to galactose 6-OH groups in keratan sulphate from a
transfer sulphate to chondroitin, chondroitin sulphate A or C, dermatan
                                                                                                                                                                                                                                                 sulphate
of about 46700. The
abelling the CDNA of
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                                                                                                                                                                6-sulpho-transferase polypeptide -
phate donor to galactose 6-hydroxy
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No. 2.2e-47;
Thes 170;
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96JP-0320535
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 29-NOV-1996;
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0 or more
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                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIP at ftp.wipo.int/pub/published_pct_sequences.
                                                                    insecticide;
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On Dec 20, 2001 this sequence version replaced gi:15627284
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Contact: hgsc-help@bcm.tmc.edu
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Pred. No. 2.2e-90;
; Mismatches 253;
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1 (bases 1 to 1989)
Lee,J.K., Bhakta,S., Rosen,S.D. and Hemme Cloning and characterization of a mammali N-acetylglucosamine-6-sulfotransferase thintestinal tissue Biochem. Biophys. Res. Commun. 263 (2), 5 99423499
2 (bases 1 to 1989)
Lee,J.-K., Bhakta,S., Rosen,S.D. and Hemm Direct Submission Submitted (10-AUG-1999) Respiratory Disea 3401 Hillview Avenue, Palo Alto, CA 94304
                    mammal
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1 (bases 1 to 139252)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J. Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
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AC095664.2 GI:179422
HTG; HTGS_PHASE1.
Norway rat.
Rattus norvegicus
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Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Verteb;
Mammalia; Eutheria; Rodentia; Sciurognathi; Mu:
1 (bases 1 to 1740)
Lee, J.K., Bhakta, S., Rosen, S.D. and Hemmerich,
Cloning and characterization of a mammalian
N-acetylglucosamine-6-sulfotransferase that is
intestinal tissue
Biochem. Biophys. Res. Commun. 263 (2), 543-54
99423499
2 (bases 1 to 1740)
Lee, J.-K., Bhakta, S., Rosen, S.D. and Hemmerich
Direct Submission
Submitted (10-AUG-1999) Respiratory Diseases,
3401 Hillview Avenue, Palo Alto, CA 94304, USA
                                                                                                                                             Diseases,
94304, US
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Pred. No. 2.2e-90;
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NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Direct Submission

Sibmitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Submitted (03-AUG-1999) Production Sequence Walnut Creek, CA 94598, USA Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598.

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598.

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598.

On Apr 25, 2001 this sequence version replaced gi:7689928.
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Consensus quality: 180040 bases at
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Homo sapiens chromosome 16 clone SEQUENCE, 17 unordered pieces.
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AC009105.7 GI:13786304
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Eukaryota; Metazoa; Chordata;

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a 'working draft' sequence. It currently
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800 Mitchell Drive, Walnut Creek, CA 94598, USA
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3401 Hillview Ave., Palo Alto, CA 94304, USA
Location/Qualifiers
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S Akama,T.O., Nishida,K., Nakayama,J., Watanabe,H., Fujiwara,T.,
Nakamura,T., Dota,A., Kawasaki,S., Inoue,Y., Maeda,N., Yamamoto,S.,
Ozaki,K., Kinoshita,S., Shimomura,Y., Tanigami,A. and Fukuda,M.N.

Macular corneal dystrophy type I and type II are caused by distinct
mutations in a new sulphotransferase gene
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N-acetylglucosamine-6-O-sulfotransferase"
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DOE Joint Genome Institute and Stanford Human Genomitted (21-DEC-2001) DOE Joint Genome Institute Drive, Walnut Creek, CA 94598, USA

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DOE Joint Genome Institute and Stanford Human Genome Lost Submitted (26-JAN-2002) DOE Joint Genome Institute Drive, Walnut Creek, CA 94598, USA
Drive, Walnut Creek, CA 94598, USA
On Jan 26, 2002 this sequence version replaced 9 Draft Sequence Produced by DOE Joint Genome Instituted (26-JAN-2002) DOE Joint Genome Instituted (26-JAN-2002)
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Santamalia; Eutheria; Primates; Catarrhini; no....

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Solicky, J.L., Hafalia, A., Burford, N., Ring, H.Z., Lal, P.,

Tribouley, C.M., Yao, M.G., Yue, H., Tang, Y.T., Patterson, C., Das, D.

Tribouley, C.M., Yao, M.G., Yue, H., Tang, Y.T., Patterson, C., Baughn, M.R.,

Sanjanwala, M.S., Gandhi, A.R., Reddy, R., Khan, F.A., Baughn, M.R.,

Ramkumar, J., Griffin, J.A. and Au-Young, J.

Brug metabolizing enzymes

Drug metabolizing enzymes

Patent: WO 0179468-A 15 25-OCT-2001;

Incyte Genomics, Inc. (US)

Location/Qualifiers

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Summary Statistics
Consensus quality: 140723 bases at least Q40
Consensus quality: 148960 bases at least Q30
Consensus quality: 151290 bases at least Q20
Consensus quality: 151290 bases at least Q20
Estimated insert size: 98000; pulse field gel estimation
Estimated insert size: 157572; sum-of-contigs estimation
Quality coverage: 7.39 in Q20 bases; pulse field gel estimation.

* NOTE: This is a 'working draft' sequence. It currently
consists of 16 contigs. The true order of the pleces
tonsists of 16 contigs. The true corder of the pleces
arbitrary. Gaps between the contigs are represented as
truns of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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DOE Joint Genome Institute.

Direct Submission

Submitted (22-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 20, 2001 this sequence version replaced gi:7711893.
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Center clone name: CITB-H1_2113H2
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Homo sapiens chromosome 5 clone C. SEQUENCE, 16 unordered pieces.
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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Butheria; Primates; Catarrhini; Hominidae; Hot bases 1 to 157337)

DoE Joint Genome Institute.

Sequencing of Human Chromosome 16
Unpublished

(Dases 1 to 157337)

DOE Joint Genome Institute.

Direct Submission

Submitted (03-N0G-1999) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA John Genome Institute.

Direct Submission

Submitted (02-NOV-2001) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA DoE Joint Genome Institute.

Direct Submission

Submitted (02-NOV-2001) Production Sequence quality, on Nov 2, 2001 this Sequence Version replaced gi:768997(
This entry has been annotated with sequence quality assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality levels above 40 are expected to have less than Base-by-base quality values are not generally visible fenBank flat file format but are available as part of this entry's Assistance.
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/rpt_type=dispersed

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TTCLL
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GlcNAc6ST expressed in small intestine and colon; s
to N-acetylglucosamine 6-0-sulfotransferase encoded
GenBank Accession Number AF176838; alternatively sp
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Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

S Akama, T.O., Mishida, K., Nakayama, J., Watanabe, H., Fujiwara, T.,

Nakamura, T., Dota, A., Kawasaki, S., Inoue, Y., Maeda, N., Yamamoto, S.,

Ozaki, K., Kinoshita, S., Shimomura, Y., Tanigami, A. and Fukuda, M.N.

Macular corneal dystrophy type I and type II are caused by distinct

mutations in a new sulphotransferase gene

L Nat. Genet. 26 (2), 237-241 (2000)

E 20472330

D 11017086

E 2 (bases I to 71503)

S Akama, T.O. and Fukuda, M.N.

Direct Submission

L Organism="Homo sapiens"

/organism="Homo sapiens"

/organism="Homo sapiens"

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/chromosome="16"

/chromosome="16"

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/chromosome="16"

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Homo sapiens intestinal N-acetylglucosamine-6-0-sulfotransfera:
(CHST5) and corneal N-acetylglucosamine-6-0-sulfotransferase
(CHST6) genes, complete cds.
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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S Akama,T.O., Nishida,K., Nakayama,J., Watanabe,H., Ozaki,K.,

Nakamura,T., Dota,A., Kawasaki,S., Inoue,Y., Maeda,N., Yamamoto,S.,

Fujiwara,T., Thonar,E.J., Shimomura,Y., Kinoshita,S., Tanigami,A.

and Fukuda,M.N.

Macular corneal dystrophy type I and type II are caused by distinct

mutations in a new sulphotransferase gene

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Akama,T.O., Nishida,K., Nakayama,J., Watanabe,H., Ozaki,K.,
Nakamura,T., Thonar,E.J.-M.A., Shimomura,Y., Kinoshita,S.,
Tanigami,A. and Fukuda,M.N.
Direct Submission
Submitted (17-MAR-2000) Glycobiology Program, The Burnham
Institute, 10901 North Torrey Pines Road, La Jolla, CA 92037, US
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Lee,J.K., Bhakta,S., Rosen,S.D. and Hemmerich,S.
Cloning and characterization of a mammalian N-acetylglucosamine-6-sulfotransferase that is hi intestinal tissue
Blochem. Blophys. Res. Commun. 263 (2), 543-549 (39423499

E 2 (bases 1 to 2170)

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S Lee,J.-K., Bhakta,S., Rosen,S.D. and Hemmerich,S.
Direct Submission

L Submitted (10-AUG-1999) Respiratory Diseases, Roc 3401 Hillview Avenue, Palo Alto, CA 94304, USA

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E 1 (bases 1 to 1462)
S Lee,J.K., Bhakta,S., Rosen,S.D. and Hemmerich,S.
Cloning and characterization of a mammalian
N-acetylglucosamine-6-sulfotransferase that is highly restricted to intestinal tissue
E Biochem. Biophys. Res. Commun. 263 (2), 543-549 (1999)
E 2 (bases 1 to 1462)
E 2 (bases 1 to 1462)
S Lee,J.-K., Bhakta,S., Rosen,S.D. and Hemmerich,S.
Direct Submission
E Submitted (10-AUG-1999) Respiratory Diseases, Roche Bioscience, linear PRI 22-SEP-1999 6-0-sulfotransferase t 0 1462 bp DNA N-acetylglucosamine complete cds. AF176839
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/organism="Mus muscu...
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_"UGGCIM0173108"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligate
with adaptors complementary to the insert adaptors and
""crtor DNA, and transformed into
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Mus
                                                                                                                                             Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
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High quality sequence stop: 433.
Location/Qualifiers
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illarity 75.5%;
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Mammalia; Eutheria;
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
(Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.,
(M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Arimura, T., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishi; Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genome Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                      Carninci, P.,
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Konno, H., Fukunishi, Y.,
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                                                                                                                                                                                                                                        /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP250022A10E10"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "
A.B. (1996), Genome Research 6(9): 791-806. "
                     Fax: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
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Pred. No. 1.5e-37;
0; Mismatches 68;
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Insert Length: 517 Std Error: 0.00
Plate: BP250022A10 row: E column:
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 517.
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FORWARD: TAATACGACTCACTATAGGG
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Location/Qualifiers
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Best Local Similarity 82.1%;
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340 Edwar
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2001

ST 04-0CT-

linear ES

clone

bp mRNA sapiens cDNA

260 bp

BI824736 603033615F1 NIH_MGC_115 Homo mRNA sequence.

DEFINITION

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/note="Organ: pooled brain, lung, testis; Vector:
    pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
    source anonymous pool of 6 male brains, age range 23-27; 1
    male lung, age 27; and 1 male testis, age 69. Library is
    oligo-dT primed and directionally cloned (EcoRV site is
    destroyed upon cloning). Average insert size 1.8 kb,
    insert size range 1-3 kb. Library is normalized and
    enriched for full-length clones and was constructed by C.
    Gruber (Invitrogen). Research Genetics tracking code
    021. Note: this is a NIH_MGC Library."
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BI824736
BI824736.1 GI:15936286
BI824736.1 GI:15936286
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
I (bases 1 to 260)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectio
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1435 row: m column: 04
High quality sequence stop: 260.
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clone UUGC1M0173108 R, DNA sequence.
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Pred. No. 1.2e-35;
); Mismatches 0;
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/organism="Homo sapiens"
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/clone="IMAGE:5174955"
/clone_lib="NIH_MGC_115"
/lab_host="DH108"
/note="Organ: pooled brair
pcMV-SPORT6; Site_1: NotI;
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quality sequence stop:
Location/Qualifiers
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Matches 260; Conservative
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Db 764 GAGTGCTTGAAAAATGCGTCGCCAAGGGTCTGCACGGGCTAAGAACGCATGCGACACC 705 Qy 505 tacagccacqtgqtgctcaaggaggtgcgcttcttcaacctgcaggtgctctacccgctg 564	684 caccaacggcaagtgggtggagccgacctcacctgcgcctgattcgcgaggtgtgccg	Db 346 CTACAAGTTGGTGGGGTCTGGAGATGACCAAGCTGGGCCAGTGGATTTACCAGGTAAC 287 Qy 924 ccacgggtcggggatcggcaagccaatcgaggccttccatacttcgtctaggaatgcgcg 983	1104 gcgtgacctcaccctgga 	RESULT 12 BF042384 LOCUS BF042384 LOCUS DEFINITION BP250022A10E10 Soares normalized bovine placenta Bos taurus cDNA clone BP250022A10E10 5', mRNA sequence. ACCESSION BF042384.1 GI:10759439 KEYWORDS EST. SOURCE COW.	ORGANISM FERENCE AUTHORS TITLE JOURNAL MMENT
Db 498 ATCCCACAAGATGAAATCATCCCCGGGCTCACTGCAGGCTCCTGTGCAGCCC 557 QY 475 ttcagcctggccgggaggcctgcctacagccacgtggtgctccaaggaggtgcgc 534	DEN bdon nigroviridis cof library G fron nce. 540. 540. 540.1 GI:8181872 genome survey sequention nigroviridis. odon nigroviridis. odon nigroviridis. odon nigroviridis.	odontidae; Tetraodon. ases 1 to 849) -Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fiau, E., Billault, A., Quetier, F., Saurin, W., Bernot, A. enbach, J. terization and repeat analysis of the compact genome water pufferfish Tetraodon nigroviridis lished ases 1 to 849) -Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fit, A., Fizames, C., Wincker, P., Brottier, P., Quetier, E., A., Fizames, C., Wincker, P., Brottier, P., Quetier, E., M., and Weissenbach, J. gene number estimate provided by genome wide analys	Tetraodon nigroviridis DNA sequen L Unpublished E 3 (bases 1 to 849) S Genoscope. Direct Submission L Submitted (12-APR-2000) to the EM This sequence is a single read an scale clone-end sequencing projec genome. For more information, ple http://www.genoscope.cns.fr/Tetra	ion/Qualifier 49 nism="Tetraod ref="taxon:99 =="129006" =_1ib="G" =_Genoscope s ri"	tch al Similarity 61.0%; Pred. No. 1.1e-38; 478; Conservative 3; Mismatches 299; gcgctgtgctcgccgcctgcagcgcctttccccgaggcac

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1. .954
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5179826"
/clone=lib="NIH_MGC_115"
/lab_host="Drgan: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
                                                  linear EST 04-OCT-2001 clone IMAGE:5179826 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 954)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectio
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11448 row: h column: 03
High quality sequence stop: 856.
Location/Qualifiers
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Hominidae;
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Pred. No. 9.4e-40;
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larity 73.9%;
Conservative
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                                             BI823850
603039012F1 NI
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BI823850.1 GI
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                                                                                                                 /- . . . . . . . . . / organism="Mus musculus" / organism="Mus musculus" / strain="C57BL" / db_xref="taxon:10090" / clone="ImAdE:1885164" / clone="ImAdE:1885164" / clone="ImAdE:1885164" / clone="ImAdE:1885164" / clone="ImAdE:1885164" / lab_host="DH10B" / lab_host="DH10B" / lab_host="DH10B" / note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); Ist strand cDNA was primed with an oligo(dT) primer [ATGTGCCTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments close it Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CGACCTGCAGGCACA."
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Pred. No. 7e-41;
); Mismatches 114;
IMAGE Consortium (info@image.llnl.gov)
MGI:969488
Seq primer: custom primer
                                                                                  ity sequence stop:
Location/Qualifiers
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Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japa (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp, Tel:81-45-503-9111, Fax:81-45-503-9170)
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB BAC Library clone:PTB-010M13.F.
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Totoki, Y., Watanabe, H. and Sakaki, Y.
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and The WashU-HHMI Mouse EST Project
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ui43c07.yl Sugano mouse embryo mewa Mus musculus cDNA clone
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/clone_lib="PTB Chimpanzee M
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medi
4444 Forest Park Parkway, Box 8501,
Tel: 314 286 1800
Fax: 314 286 1810
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DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
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sequence.

ACCESSION AL248380.

VERSION AL248380.1 GI:7969392

KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
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1 (bases 1 to 1067)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jaillon,O., Dasilva,C., Fizames,C.,
t,A., Quetier,F., Saurin,W., Bernot,
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P., Brottier,P.,
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                                                                                                                         Charaterization and repeat analysis of the cafreshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Tetraodon nigroviridis'/db_xref="taxon:99883"
/clone="033J20"
/clone_lib="G"
/note="Genoscope sequence ID : COF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346.4; DB 12;
No. 1.8e-50;
                                                                                                                                                Unpublished
2 (bases 1 to 1067)
Roest-Crollius, H., Jaillon, O., Dasilva, C.
Bernot, A., Fizames, C., Wincker, P., Brotti
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by ge
Tetraodon nigroviridis DNA sequence
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Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Kumamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Yamamoto,R., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Koheda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Koheda,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
E 20530913
D 11076861
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

Nature 409, 685-690 (2001)

Nature 409, 685-690 (2001)

Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kosukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
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AK009113.1 GI:12843701
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:2310003G18.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus adult male tongue cDNA, RIKEN full-length enriche library, clone:2310003G18:carbohydrate (chondroitin 6/keratan) sulfotransferase 4, full insert sequence.
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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/brotein_id="BAB26078.1"
/db_xref="GI:12843702"
/translation="MMLLKKGRLLMFLGSQVIVVALFIHMSVHRHLSQREESRRPVHV
LVLSSWRSGSSFVGQLFGQHPDVFYLMEPAWHVWMTFTSSTAWKLHMAVRDLLRSVFL
CDMSVFDAYMNPGPRKQSSLFQWEQSRALCSAPVCDFFPAHEISSPKHCKLLCGQQPF
DMVEKACRSHGFVVLKEVRFLSLQALYPLLTDPSLNLHVVHLVRDPRAVFRSREHTTI
ELMVDSHIVLGQHLETIKEEDQPYYAMKIICKSQVDIVKAIQTLPEALQQQRYLFLRYE
DLVRAPLAQTTRLYKFVGLDFLPHLQTWVYNVTRGKGMGQHAFHTNARNALNVSQAWR
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Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I.,
Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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Pred. No. 1.7e-51;
. wiematches 386;
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/clone_lib="RIKEN full-length e
/dev_stage="adult"
96. .1262
/gene="Chst4"
96. .1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / cryanism="Mus musculus"
/strain="C57BL/6J"
/db_xref="MGD:MGI:1904558"
/db_xref="taxon:10090"
/clone="2310003G18"
/sex="male"
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                                                                                                                                      /dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M Fatima Bonaldo. "
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www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 917 Std Error: 0.00
Seg primer: -400P from Gibco
                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2405856"
/clone_lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinodifferentiated (4 pooled tumors, in metastatic)"
                                                                                                                                                                                                                                                                                    Score 487.6; DB 9;
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436 bp mRNA linear EST 14-OCT-1999 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2586803 3'TR:088199 O88199 CHONDROITIN 6-SULFOTRANSFERASE.;, mRNA
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/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Normalized to Cot 500. Average insert size 1.11kb.
Normalized version of NCI_CGAP_Co18. Library constructed by Life Technologies."
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A Library Preparation: Life
Arrayed by: Christa Prange, Tha
Acing by: Washington University
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 436)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CG Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Mi
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, "I.M.A.G.E. Consortium DNA Sequencing by: Washington Universi
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 431.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2586803"
/clone_lib="NCI_CGAP_Co2(
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3642903"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library
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Homoo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostumi,

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 525)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

U npublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Centaction distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL, send email to:
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7084a08.xl NCI_CGAP_Kid11 Homo sapiens cDNA clone similar to TR:Q9UBY3 Q9UBY3 N-ACETYLGLUCOSAMINE 6-0-SULFOTRANSFERASE.;, mRNA sequence.
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info@image.llnl.gov
High quality sequence stop: '
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wj46c01.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2405856 3 similar to TR:075667 075667 DJ71L16.4; contains PTR5.b2 PTR5 AI824100
AI824100.1 GI:5444771
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 620)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy ProTumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Secondary Secondary Mashington University Genome Secondary Arrayed by: Washington University Genome Secondary Arrayed by: Washington University Genome Secondary Arrayed Butto Scares Arrayed Butto University Genome Scares Arrayed Butto Scares Arrayed But
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1 (bases 1 to 735)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurol
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
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                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. I
Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.,
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CLone distribution: NCI-CGAP clone distribution in:

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SUMMARIES

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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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TISSUE=BRAIN;
Uchimura K., Muramatsu T.;
"Identification and molecular characterization of novel N-acetylglucosamine-6-0-sulfotransferase.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ dat EMBL; AL022165; CAA18154.1;
EMBL; AB040711; BAB13770.1; -.
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STRAIN=C57BL/6J; TISSUE=EMBRYO;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

Schriml L.M., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Chors P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
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Bhakta S., Bartes A., Bowman K.G., Kao W.M., Polsky I., Lee J.-K., Cook B.N., Bruehl R.E., Rosen S.D., Bertozzi C.R., Hemmerich S.; "Sulfation of N-Acetylglucosamine by Chondroitin 6-Sulfotransferase (GST-5).";
J. Biol. Chem. 275:40226-40234(2000).
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Mus
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RAVASSRIRSRHGLIRESLQVVRSRDPRAHRMPFLEAAGHKLGAKKEGVGGPADYHALGA
                                                                                             -NGIVLGTNGKWV--EADPH-LRL
                                          D--VCKTLCTROPFSLAREACRSYSHVVLKEVRFFNLQVLYPLLSDPALNLRIVHLVRDP
                                                                                                                                                                                                                                                                                                                                                                 O9EP78;
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
N-ACETYLGLUCOSAMINE 6-O-SULFOTRANSFERASE GST-5 (N-ACETYLGLUCOSAMINE-6-O-SULFOTRANSFERASE) (2600013M07RIK PROTEIN).
CHST7 OR GST5 OR 2600013M07RIK.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                --REAAGPILARD-
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Q9EP78
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Murinae; Mu
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Sciurognathi; Muridae;
                                                                                                                     CRC64
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHONDROITIN 6-SULFOTRANSFERASE-2.
CHST7 OR MC6ST-2.
Mus musculus (Mouse).
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                           CDNA
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Pred. No. 1.8e-49;
; Mismatches 126;
  Kawaji
                                                                                                                                                         11;
                                                                                                                                                         Score 617.5; DB 11
Pred. No. 9.1e-50;
; Mismatches 126;
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TISSUE=MAMMARY GLAND;
Kitagawa H., Uyama T., Sugahara K.;
"Cloning and Expression of Mouse Chondroitin f
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ
EMBL; AB046929; BAB40372.1; -.
MGD; MGI:1891767; Chst7.
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                              mouse
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Chordata;
Rođentia;
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Wynshaw-Boris A., Yoshida K., Hayashizaki Y.;
"Functional annotation of a f Nature 409:685-690(2001).
EMBL; AF280089; AAG48247.1; EMBL; AB040710; BAB13769.1; EMBL; AK011202; BAB27465.1; AGD; MGI:1891767; Chst7.
Transferase.
SEQUENCE 484 AA; 54766 MW;
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38.8%;
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il Similarity 39.1%;
147; Conservative
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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146; Conser
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                                                                                                                                                                                    Length
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Catarrhini; Hominidae; Homo
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                                                                                                                                                                          Score 659.5; DB 4;
Pred. No. 1.1e-53;
; Mismatches 122;
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01-MAY-2000 (Trembirel, 13, Created)
01-MAY-2000 (Trembirel, 13, Last sequence un
01-DEC-2001 (Trembirel, 19, Last annotation
N-ACETYLGIUCOSAMINE-6-0-SULFOTRANSFERASE (GI
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Genomics 55:345-347(1999).

EMBL; AF083066; AAD20981.1; -.

InterPro; IPR000863; Sulfotransferase
Pfam; PF00685; Sulfotransfer; 1.

Transferase.

SEQUENCE 530 AA; 57857 MW; A82Ca2
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EMBL; AB014679; BAA34265.1; -...
InterPro; IPR000863; Sulfotransferase.

Pfam; PF00685; Sulfotransfers.
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MEDLINE=98391845; PubMed=9722682;
MEDLINE=98391845; PubMed=9722682;
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                                                                                                              57857 MW;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                   Match 32.2%;
Local Similarity 39.1%;
Nes 151; Conservative
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Transferase.
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Best Local S
Matches 151
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                            -AFFNWATSRALCSPPACSAFPRGTISKQ
                                                                                D--VCKTLCTRQPFSLAREACRSYSHVVLKEVRFFNLQVLYPLLSDPALNLRIVHLVRDP
                                                                                                                         -NGIVLGTNGKWV--EADPH-LRL
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EMBL; AB014680; BAA34266.1; ...
InterPro; IPR000863; Sulfotransferase.

Pfam; PF00685; Sulfotransfer; 1.
                Indels
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Catarrhini; Hominidae;
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
   Pred. No. 1.9e~53;
; Mismatches 121;
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2-53;
121;
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Pred. No. 2.2e-5
8; Mismatches 1
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natsu H., Kaname
                                                                                                                                                     -REAAGPILARD~
            68;
                                                                    VRDLMRSIFLCDMDVFDAYMPQ--
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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Best Local Similarity 39.7%;
Matches 149; Conservative
Similarity 39. 9; Conservative
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VNSPEEVKDLSKTLL
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TISSUE=BRAIN;
MEDLINE=98391845; E
Uchimura K., Murama
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Q9Y4C5;
01-NOV-1999
01-NOV-1999
01-DEC-2001
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Query Match

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Mus
                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                        MRSIFLCDMDVFDAYMPQ---SRNLS--AFFNWATSRALCSPPACSAFPRGTISKQD
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                                                                                                                                                                            Kurosawa
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Q9GZN5;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
N-ACETYLGLUCOSAMINE 6-O-SULFOTRANSFERASE.
Homo sapiens (Human).
                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE=WHOLE EMBRYOS;

MEDLINE=98380482; PubMed=9712885;

Wchimura K., Muramatsu H., Kadomatsu K., Fan Q., Kur

Witsucka C., Kannagi R., Habuchi O., Muramatsu T.;

Mitsucka C., Kannagi R., Habuchi O., Muramatsu T.;

Mitsucka C., Kannagi R., Habuchi O., Muramatsu T.;

Molecular cloning and characterization of an N-acet

sulfotransferase.";

J. Biol. Chem. 273:22577-22583(1998).

EMBL; AB011452; BAA32138.1; -.

EMBL; AB011452; BAA32139.1; -.

EMBL; AB011451; BAA32137.1; -.
                 088276;
088276;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
N-ACETYLGLUCOSAMINE-6-0-SULFOTRANSFERASE LONG FORM
                                                                                                                                                                                                                                                                                                                                                            121;
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Matches 150;
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an N-acetyllactosamine
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   Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPPAC
                                                                                                                                                                                                                                                                                                                                                                                                       -GEDRVHVLVLSSWRSGSSFLGQLFSQHPDVFYLMEPAWHVWTTL
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Euteleostomi
                                                                                                                                                                                                                                                                                                  \Omega
                                                                                                                                                                                                                                                                                                                                                                                      -SRNLS--AFFNWATSRALC
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                                                                                                                 of human N-
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on update)
  Vertebrata; |
; Hominidae;
                                                                                                                                                                                                                                                                                                     122;
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                                                                                                                                                                                                                                E27797D44931BA18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "CHST1 and CHST2 sulfotransferases expressed endothelial cells: cDNA cloning, expression, localization.";
                                                                                                                                                                                                                                                                         659.5; DB
No. 1e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence uk
(TrEMBLrel. 19, Last annotation
; SULFOTRANSFERASE 2.
                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=PLACENTA;
MEDLINE=20498786; PubMed=11042394;
Sakaguchi H., Kitagawa H., Sugahara K.;
Sakaguchi H., Kitagawa H., Sugahara K.;
"Functional expression and genomic structure
"Functional expression and genomic structure
acetylglucosamine-6-0-sulfotransferase that t
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Catarrhini;
                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                530
     Craniata; Ve
Catarrhini;
                                                                                                                                                                sequence.";
Biochim. Biophys. Acta 1523:269-276(2000)
EMBL; AB021125; BAB16887.1; -.
EMBL; AB021124; BAB16886.1; -.
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SEQUENCE FROM N.A.
TISSUE=UMBILICAL VEIN ENDOTHELIAL CI
MEDLINE=99168906; Pubmed=10049591;
Li X., Tedder T.F.;
"CHST1 and CHST2 sulfotransferases
"CHST1 and CHST2 sulfotransferases
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                        68;
    Chordata;
Primates;
                                                                                                                                                                                                                                   MM;
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39.1%;
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                                                                                                                                                                                                                                                                                                          Conservative
  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                   al Similarity
151; Concorr
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Q9Y6F2;
01-NOV-1999 (
01-NOV-1999 (
01-DEC-2001 (
CARBOHYDRATE )
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SEQUENCE
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Best Local S
Matches 151
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Eukaryota;
Mammalia;
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SEQUENCE
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MGD; 1
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Q9WUE5;
Q9WUE5;
O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
N-ACETYLGLUCOSAMINE 6-O-SULFOTRANSFERASE (CARBOHYDRATE (CHONDROITIN 6/KERATAN) SULFOTRANSFERASE 4).
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                         Euteleostomi;
Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                Yeh
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MEDLINE=99361934; PubMed=10435581;
Miraoka N., Petryniak B., Nakayama J., Tsuboi S., Suzuki M., Ye Izawa D., Tanaka T., Miyasaka M., Lowe J.B., Fukuda M.;
"A novel, high endothelial venule-specific sulfotransferase exp 6-sulfo sialyl Lewis(x), an L-selectin ligand displayed by CD34 Immunity 11:79-89(1999).
EMBL; AF109155; AAD45579.1; -.
MGD; MGI:1349479; Chst4.
Transferase; Lectin; Selectin.
SEQUENCE 388 AA; 44636 MW; 6D5371AFB6884AEE CRC64;
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                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
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                                                                                                                                                                                       Last sequence up
Last annotation
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              \mathcal{G}_{\mathcal{G}}
                                                                                                                                    388
             LGYRPVYSADQQRDLTLDLVLPRGPDHFSWASPD
                                               STWTVPE
                                                                                                                                                                      Created)
                                                                                                                              O9R111;
O9R111;
O1-MAY-2000 (TrEMBLrel. 13, Create)
01-MAY-2000 (TrEMBLrel. 13, Last soll-DEC-2001 (TrEMBLrel. 19, Last s
                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cı
Mammalia; Eutheria; Rodentia; Sc
NCBI_TaxID=10090;
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55.9%;
                              Conservative
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194; Conser
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SEQUENCE FROM N.A.

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STRAIN=257BL/61; TISSUE=TONGUE;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Mayashizaki Y.,

Functional annotation of a full-length mouse cDNA collection.";

Brat. A Para Matsus A., Poshida R., Hasegawa Y., Kawaji H., Kohtsuki S.,

Brat. A Payashizaki Y.,

Brat. A Para Matsuki Y.,

Brat. A Payashizaki Y.,

Brat. A Payashiz
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      Euteleost
Murinae;
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                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=TONSIL;
MEDLINE=99264336; Pubmed=10330415;
Bistrup A., Bhakta S., Lee J.-K., Belov Y.Y., Gunn M.D., Huang C.-C., Kannagi R., Rosen S.D., Hemmerich S.;
"Sulfotransferases of two specificities function in the of high endothelial cell ligands for L-selectin.";
J. Cell Biol. 145:899-910(1999).
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      ertebrata; i; Muridae;
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Pred. No. 4.7e-82;
; Mismatches 87;
Craniata; Vert
Sciurognathi;
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AF131236; AAD33016.1; -.
AK009113; BAB26078.1; -.
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   Chordata;
Rodentia;
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Best Local Similarity 55.6%;
Matches 193; Conservative
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   Metazoa;
Eutheria;
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                                                        NCBI_TaxID=10090;
[1]
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NCBI_TaxID=9606;
[1]
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SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=INTESTINE;
MEDLINE=99423499; PubMed=10491328;
Lee J.-K., Bhakta S., Rosen S.D., Hemmerich S.;
Lee J.-K., Bhakta S., Rosen S.D., Hemmerich S.;
"Cloning and Characterization of a Mammalian N-Acetylglucoss Sulfotransferase that is Highly Restricted to Intestinal Tissulfotrensferase that is Highly Restricted to Intestinal Tissulchem. Biophys. Res. Commun. 263:543-549(1999).
EMBL; AF176841; AAD56002.1; -.
EMBL; AF176840; AAD56002.1; -.
MGD; MGI:1931825; Chst5.
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Pred. No. 1.5e-136;
0; Mismatches 62;
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                                                                                                                         Last sequence up
Last annotation
                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Ver'
Mammalia; Eutheria; Rodentia; Sciurognathi;
NCBI_TaxID=10090;
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6-O-SULFOTRANSFERASE.
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SVHSELEQRDLSLDLLLPRGMDSFKWAS
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t Local Similarity 76.0%;
ches 295; Conservative
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
N-ACETYLGLUCOSAMINE 6-O-
CHST5 OR I-GLCNAC-6-ST.
Mus musculus (Montan)
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MEDLINE=21332592; PubMed=11439191;
Yeh J.-C., Hiraoka N., Petryniak B., Nakayama J., Ellies L.G. Yeh J.-C., Hindsgaul O., Marth J.D., Lowe J.B., Fakuda M.;
Rabuka D., Hindsgaul O., Marth J.D., Lowe J.B., Fakuda M.;
"Novel sulfated lymphocyte homing receptors and their control corel extension betal, 3-N-acetylglucosaminyltransferase.";
Cell 105:957-969(2001).

EMBL; AF131235; AAD33015.1; -.

R EMBL; AF149783; AAK48417.1; -.

R EMBL; AF149783; HLH_Myc.

R PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

Transferase; Lectin; Selectin.

Transferase; Lectin; Selectin.

Transferase; Lectin; Selectin.
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                                                                                                                                       Vertebrata;
; Hominidae;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=TONSIL;
MEDLINE=99264336; PubMed=10330415;
Bistrup A., Bhakta S., Lee J.K., Belov Y.Y., Gunn M. Huang C.C., Kannagi R., Rosen S.D., Hemmerich S.;
"Sulfotransferases of two specificities function in of high endothelial cell ligands for L-selectin.";
J. Cell Biol. 145:899-910(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                         Galactose/N-Acetylgalactosamine/N-Acetylglucosamine Sulfotransferase Gene Family."; Glycobiology 0:0-0(2001).
               12, Created)
12, Last sequence update)
19, Last annotation update)
--SULFOTRANSFERASE (L-SELECTI)
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9.9e-87;
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Mismatches
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Catarrhini;
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Pred. No. 9
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Primates;
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Q9Y5R3;
01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
N-ACETYLGLUCOSAMINE 6-O-S
SULFOTRANSFERASE GST-3).
GST3.
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Eukaryota; Metazoa
Mammalia; Eutheria
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se Y., Maeda l
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Q1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-OCT-2001 (TrEMBLrel. 18, Last annotation updat INTESTINAL GLCNAC-6-SULFOTRANSFERASE (INTESTINAL ACETYLGLUCOSAMINE-6-O-SULFOTRANSFERASE).
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Mismatches
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gene.
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Catarrhini;
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SEQUENCE FROM N.A.
MEDLINE=20472330; PubMed=11017086;
Akama T.O., Nishida K., Nakayama J., Wata
Nakamura T., Dota A., Kawasaki S., Inoue
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MEDLINE=20472330; PubMed=11017086;

Akama T.O., Nishida K., Nakayama J., Watanabe H., Fujiwara T.,

Akamura T., Dota A., Kawasaki S., Inoue Y., Maeda N., Yamamoto S.,

Nakamura T., Dota A., Rawasaki S., Inoue Y., Maeda N., Yamamoto S.,

Nakamura T., Dota A., Rawasaki S., Inoue Y., Maeda N., Yamamoto S.,

Natamura T., Shimomura Y., Tanigami A., Fukuda M.N.;

I macular corneal dystrophy type I and type II are caused by distinc

mutations in a new sulphotransferase gene.";

Nat. Genet. 26:237-241(2000).

REMBL; AF219990; AAG26325.1; -.

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N-ACETYLGLUCOSAMINE 6-O-SULFOTRANSFERASE GST-4BETA (CONGRAYBETA OR CHST6.

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S HOMO sapiens (Human).

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SUMMARIES

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